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(54) Title: NOVEL G PROTEIN-COUPLED RECEPTORS

(57) Abstract: The present invention provides a gene encoding a G protein-coupled receptor termed nGPCR-x; constructs and recombinant host cells incorporating the genes; the nGPCR-x polypeptides encoded by the gene; antibodies to the nGPCR-x polypeptides; and methods of making and using all of the foregoing.

SEQ ID NO:79, SEQ ID NO:81 SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:89,
SEQ ID NO:93 and SEQ ID NO:185.

8. The isolated nucleic acid molecule of claim 1 wherein said nucleic acid
5 molecule is DNA.
9. The isolated nucleic acid molecule of claim 1 wherein said nucleic acid
molecule is RNA.
10. 10. An expression vector comprising a nucleic acid molecule of any one of claims
1 to 5.
11. The expression vector of claim 10 wherein said nucleic acid molecule
comprises a sequence selected from the group of odd numbered sequences consisting
15 of SEQ ID NO:1 to SEQ ID NO:93 and SEQ ID NO:185.
12. The expression vector of claim 10 wherein said nucleic acid molecule
comprises a nucleotide sequence selected from the group consisting of: SEQ ID
NO:1, SEQ ID NO:73, SEQ ID NO:9, SEQ ID NO:77, SEQ ID NO:11, SEQ ID
20 NO:79, SEQ ID NO: 21, SEQ ID NO:81 SEQ ID NO:53, SEQ ID NO:83, SEQ ID
NO:59, SEQ ID NO:85, SEQ ID NO:63, SEQ ID NO:87, SEQ ID NO:89, SEQ ID
NO:67, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO: 3, and SEQ ID NO: 185.
13. The expression vector of claim 10 wherein said nucleotide sequence is
25 selected from the group consisting of: SEQ ID NO: 73, SEQ ID NO:77, SEQ ID
NO:79, SEQ ID NO:81 SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:89, SEQ ID
NO:93 and SEQ ID NO: 185.
14. The expression vector of claim 10 wherein said vector is a plasmid.
- 30 15. The expression vector of claim 10 wherein said vector is a viral particle.
16. The expression vector of claim 15 wherein said vector is selected from the
group consisting of adenoviruses, baculoviruses, parvoviruses, herpesviruses,

SEQ ID NO:78; SEQ ID NO:80; SEQ ID NO:82; SEQ ID NO:84; SEQ ID NO: 86;
SEQ ID NO:90; and SEQ ID NO:94.

- 5
60. The method of claim 57 wherein said activity is neuropeptide binding.
61. The method of claim 57 wherein said activity is neuropeptide signaling.
62. A compound identified by the method of claim 57.
- 10 63. A method of identifying an animal homolog of nGPCR-x comprising the steps:
- a) comparing the nucleic acid sequences of the animal with a sequence selected from the group of odd numbered sequence consisting of SEQ ID NO: 1 to SEQ ID NO: 93, SEQ ID NO: 185, and portions thereof, said portions being
- 15 at least 10 nucleotides; and
- b) identifying nucleic acid sequences of the animal that are homologous to said sequence selected from the group of odd numbered sequence consisting of SEQ ID NO: 1 to SEQ ID NO: 93, SEQ ID NO: 185, and portions thereof.
- 20
64. The method of claim 63 wherein comparing the nucleic acid sequences of the animal with a sequence selected from the group of odd numbered sequence consisting of SEQ ID NO: 1 to SEQ ID NO: 93, SEQ ID NO: 185, and portions thereof, said portions being at least 10 nucleotides is performed by DNA hybridization.
- 25
65. The method of claim 63 wherein comparing the nucleic acid sequences of the animal with a sequence selected from the group of odd numbered sequence consisting of SEQ ID NO: 1 to SEQ ID NO: 93, SEQ ID NO: 185, and portions thereof, said portions being at least 10 nucleotides is performed by computer homology search.
- 30
66. A method of screening a human subject to diagnose a disorder affecting the brain or genetic predisposition therefor, comprising the steps of:
- (a) assaying nucleic acid of a human subject to determine a presence or an absence of a mutation altering an amino acid sequence, expression, or biological

(c) performing a polynucleotide migration assay to determine whether nucleic acid from the human subject has a nucleotide sequence identical to or different from one or more reference sequences; and

(d) performing a restriction endonuclease digestion to determine
5 whether nucleic acid from the human subject has a nucleotide sequence identical to or different from one or more reference sequences.

71. A method according to claim 70 wherein the assaying step comprises:
performing a polymerase chain reaction assay to amplify nucleic acid comprising
10 nGPCR-40 or nGPCR-54 coding sequence, and determining nucleotide sequence of the amplified nucleic acid.

72. A method of screening for an nGPCR-40 or nGPCR-54 hereditary schizophrenia genotype in a human patient, comprising the steps of:

15 (a) providing a biological sample comprising nucleic acid from said patient, said nucleic acid including sequences corresponding to alleles of nGPCR-40 or nGPCR-54; and

(b) detecting the presence of one or more mutations in the nGPCR-40 allele or the nGPCR-54 allele;

20 wherein the presence of a mutation in an nGPCR-40 allele or nGPCR-54 allele is indicative of a hereditary schizophrenia genotype.

73. The method according to claim 72 wherein said biological sample is a cell sample.

25

74. The method according to claim 72 wherein said detecting the presence of a mutation comprises sequencing at least a portion of said nucleic acid, said portion comprising at least one codon of said nGPCR-40 or nGPCR-54 alleles.

30 75. The method according to claim 72 wherein said nucleic acid is DNA.

76. The method according to claim 72 wherein said nucleic acid is RNA.

28. The nucleic acid molecule of claim 27 wherein said molecule is an antisense oligonucleotide directed to a region of a sequence selected from the group of odd numbered sequences consisting of SEQ ID NO:1 to SEQ ID NO:93 and SEQ ID NO:
5 185.

29. The nucleic acid molecule of claim 28 wherein said oligonucleotide is directed to a regulatory region of a sequence selected from the group of odd numbered sequences consisting of SEQ ID NO:1 to SEQ ID NO:93 and SEQ ID NO:185.

10

30. The nucleic acid molecule of claim 27 wherein said molecule is an antisense oligonucleotide directed to a region of nucleotide sequence selected from the group consisting of: SEQ ID NO: 73, SEQ ID NO:77, SEQ ID NO:79; SEQ ID NO:81 SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:89, SEQ ID NO:93 and SEQ ID NO: 185.

15

31. A composition comprising a nucleic acid molecule of any one of claims 1 to 5 or 27 and an acceptable carrier or diluent.

32. A composition comprising a recombinant expression vector of claim 10 and an
20 acceptable carrier or diluent.

33. A method of producing a polypeptide that comprises a sequence selected from the group of even numbered sequences consisting SEQ ID NO: 2 to SEQ ID NO: 94 and SEQ ID NO: 186, and homologs and fragments thereof, said method comprising
25 the steps of:

- a) introducing a recombinant expression vector of claim 10 into a compatible host cell;
- b) growing said host cell under conditions for expression of said polypeptide; and
- 30 c) recovering said polypeptide.

34. The method of claim 33 wherein said host cell is lysed and said polypeptide is recovered from the lysate of said host cell.

43. A composition comprising a polypeptide of claim 36 and an acceptable carrier or diluent.
- 5 44. An isolated antibody which binds to an epitope on a polypeptide of claim 36.
45. The antibody of claim 44 wherein said antibody is a monoclonal antibody.
46. A composition comprising an antibody of claim 44 and an acceptable carrier
10 or diluent.
47. A method of inducing an immune response in a mammal against a polypeptide of claim 36 comprising administering to said mammal an amount of said polypeptide sufficient to induce said immune response.
- 15 48. A method for identifying a compound which binds nGPCR-x comprising the steps of:
- a) contacting nGPCR-x with a compound; and
 - b) determining whether said compound binds nGPCR-x.
- 20 49. The method of claim 48 wherein the nGPCR-x comprises an amino acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 74; SEQ ID NO: 4, SEQ ID NO: 186; SEQ ID NO: 10, SEQ ID NO: 78; SEQ ID NO: 12, SEQ ID NO: 80; SEQ ID NO: 22, SEQ ID NO: 82; SEQ ID NO: 54, SEQ ID NO: 84; SEQ
25 ID NO: 60, SEQ ID NO: 86; SEQ ID NO: 64, SEQ ID NO: 88, SEQ ID NO: 90; SEQ ID NO: 68, SEQ ID NO: 92, and SEQ ID NO: 94.
50. The method of claim 48 wherein the nGPCR-x comprises an amino acid sequence selected from the group consisting of: SEQ ID NO: 74; SEQ ID NO: 186;
30 SEQ ID NO: 78; SEQ ID NO: 80; SEQ ID NO: 82; SEQ ID NO: 84; SEQ ID NO: 86; SEQ ID NO: 90; and SEQ ID NO: 94.
51. The method of claim 48 wherein binding of said compound to nGPCR-x is determined by a protein binding assay.

80. A purified and isolated polynucleotide comprising a nucleotide sequence encoding an nGPCR-40 or nGPCR-54 allelic variant identified according to claim 79.
81. A host cell transformed or transfected with a polynucleotide according to
5 claim 80 or with a vector comprising the polynucleotide.
82. A purified polynucleotide comprising a nucleotide sequence encoding nGPCR-40 or nGPCR-54 of a human with schizophrenia;
wherein said polynucleotide hybridizes to the complement of SEQ ID
10 NO:83 or of SEQ ID NO:85 under the following hybridization conditions:
(a) hybridization for 16 hours at 42°C in a hybridization solution comprising 50% formamide, 1% SDS, 1 M NaCl, 10% dextran sulfate and
(b) washing 2 times for 30 minutes at 60°C in a wash solution comprising 0.1x SSC and 1% SDS; and
15 wherein the polynucleotide that encodes nGPCR-40 or nGPCR-54 amino acid sequence of the human differs from SEQ ID NO:84 or SEQ ID NO:86 by at least one residue.
83. A vector comprising a polynucleotide according to claim 82.
20
84. A host cell that has been transformed or transfected with a polynucleotide according to claim 82 and that expresses the nGPCR-40 or nGPCR-54 protein encoded by the polynucleotide.
- 25 85. A host cell according to claim 84 that has been co-transfected with a polynucleotide encoding the nGPCR-40 or nGPCR-54 amino acid sequence set forth in SEQ ID NO:84 or SEQ ID NO:86 and that expresses the nGPCR-40 or nGPCR-54 protein having the amino acid sequence set forth in SEQ ID NO:84 or SEQ ID NO:86.
- 30 86. A method for identifying a modulator of biological activity of nGPCR-40 or nGPCR-54 comprising the steps of:
a) contacting a cell according to claim 84 in the presence and in the absence of a putative modulator compound;

90. An method according to claim 89 wherein the composition comprises a cell transformed or transfected with a polynucleotide that encodes nGPCR-40 or nGPCR-54.

5 91. A method of purifying a G protein from a sample containing said G protein comprising the steps of:

a) contacting said sample with a polypeptide of claim 1 for a time sufficient to allow said G protein to form a complex with said polypeptide;

b) isolating said complex from remaining components of said
10 sample;

c) maintaining said complex under conditions which result in dissociation of said G protein from said polypeptide; and

d) isolating said G protein from said polypeptide.

15 92. The method of claim 91 wherein said sample comprises an amino acid sequence selected from the group of even numbered sequences consisting of SEQ ID NO:2 to SEQ ID NO:94 and SEQ ID NO:186.

93. The method of claim 91 wherein said polypeptide comprises an amino acid
20 sequence homologous to a sequence selected from the group of even numbered sequences consisting of SEQ ID NO:2 to SEQ ID NO:94 and SEQ ID NO:186.

94. The method of claim 91 wherein said polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 74; SEQ
25 ID NO: 4, SEQ ID NO: 186; SEQ ID NO:10, SEQ ID NO:78; SEQ ID NO:12, SEQ ID NO:80; SEQ ID NO: 22, SEQ ID NO:82; SEQ ID NO:54, SEQ ID NO:84; SEQ ID NO:60, SEQ ID NO: 86; SEQ ID NO:64, SEQ ID NO: 88, SEQ ID NO:90; SEQ ID NO:68, SEQ ID NO: 92, and SEQ ID NO:94.

30 95. The method of claim 91 wherein said polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NO: 74; SEQ ID NO: 186; SEQ ID NO:78; SEQ ID NO:80; SEQ ID NO:82; SEQ ID NO:84; SEQ ID NO: 86; SEQ ID NO:90; and SEQ ID NO:94.

SEQUENCE LISTING

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Vogeli, Gabriel
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Sejlitz, Torsten
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Slightom, Jerry
Schellin, Kathleen
Bannigan, Chris
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Ser Val Ile Phe Met Ile Asn Leu Ser Val Thr Asp Leu Met Leu Ala
50 55 60

Ser Val Leu Pro Phe Gln Ile Tyr Tyr His Cys Asn Arg His His Trp
65 70 75 80

Val Phe Gly Val Leu Cys Asn Leu Val Val Thr Val Ala Phe Tyr Ala
85 90 95

Asn Met Tyr Ser Ser Ile Leu Thr Met Thr Cys Ile Ser Val Glu Arg
 100 105 110
 Phe Leu Gly Ile Leu Tyr Pro Leu Ser Ser Lys Arg Trp Arg Arg Arg
 115 120 125
 Arg Tyr Ala Val Ala Ala Cys Ala Gly Thr Trp Leu Leu Leu Leu Thr
 130 135 140
 Ala Leu Ser Pro Leu Ala Arg Thr Asp Leu Thr Tyr Pro Val His Ala
 145 150 155 160
 Leu Gly Ile Ile Thr Cys Phe Asp Val
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<210> 9
 <211> 270
 <212> DNA
 <213> H.Sapiens

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 gcacgggagg gaggcgtctt cgtggcactc actgcgtccg tgctgagcct cctgggcatac 180
 gcgctggagc gcagcctcac catggcgcg cagggggccc cgcccgtctc cagtcggggg 240
 cgcacgctgg cgatggcagc cgcggcctgg 270

<210> 10
 <211> 90
 <212> PRT
 <213> H.Sapiens

<400> 10
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 Gly Ala Ala Tyr Ala Ala Asn Ile Leu Leu Ser Gly Pro Leu Thr Leu
 20 25 30
 Lys Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu Gly Gly Val Phe Val
 35 40 45
 Ala Leu Thr Ala Ser Val Leu Ser Leu Leu Gly Ile Ala Leu Glu Arg
 50 55 60
 Ser Leu Thr Met Ala Arg Arg Gly Pro Ala Pro Val Ser Ser Arg Gly
 65 70 75 80
 Arg Thr Leu Ala Met Ala Ala Ala Ala Trp
 85 90

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 <211> 888

<212> DNA
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 gatttccctc ttatgatctg cctgcctttt cggacagact attacctcag acgtagacac 180
 tgggcttttg gggacattcc ctgccgagtg gggctcttca cgttggccat gaacagggcc 240
 gggagcatcg tgttccttac ggtggtggct gcggacaggt atttcaaagt ggtccacccc 300
 caccacgcgg tgaacactat ctccaccccg gtggcggctg gcatcgtctg caccctgtgg 360
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 acggcgcgtc cctgtgagag cttcatcatg gagtcggcca atggctggca tgacatcatg 480
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 cacataaccc tcagcttcac ctacatgaac agcatgctgg atcccctggt gtattatttt 780
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 <212> PRT
 <213> H.Sapiens

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 20 25 30
 Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu Met Ile Cys Leu
 35 40 45
 Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His Trp Ala Phe Gly
 50 55 60
 Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala Met Asn Arg Ala
 65 70 75 80
 Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp Arg Tyr Phe Lys
 85 90 95

Val Val His Pro His His Ala Val Asn Thr Ile Ser Thr Arg Val Ala
 100 105 110

Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile Leu Gly Thr Val
 115 120 125

Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu Thr Ala Val Ser
 130 135 140

Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp His Asp Ile Met
 145 150 155 160

Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile Leu Phe Cys Ser
 165 170 175

Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln Leu Ala Arg Gln
 180 185 190

Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val Val Ala Ile Val
 195 200 205

Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg Leu Tyr Phe Leu
 210 215 220

Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val His Gly Ala Leu
 225 230 235 240

His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met Leu Asp Pro Leu
 245 250 255

Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe Tyr Asn Lys Leu
 260 265 270

Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His Ser Lys Thr Gln
 275 280 285

Arg Pro Glu Glu Met Pro Ile Ser
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<210> 13
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 tgcaagctgg tgcacttcct gttctatata aacctttacg gcagcatcct gctgctgacc 180
 tgcattctctg tgcaccagtt cctaggtgtg tgccacccac tgtgttcgct gccctaccgg 240
 acccgagcaggc atgcctggct gggcaccagc accacctggg ccctgggtgg cctccagctg 300
 ctgcccacac tggccttctc ccacacggac tacatcaatg gccagatgat ctggtatgac 360
 atgaccagcc aagagaattt tgatcggtt tttgcctacg gcatagttct gacattgtct 420

ggctttcttt ccctccttgg tcattttggt gtgctattca ctgatgggtca ggagcctgat 480
 caagccagag gagaacctca tgaggacagg 510

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 <212> PRT
 <213> H.Sapiens

<400> 14

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 20 25 30
 Arg Trp Pro Phe Gly Glu Leu Leu Cys Lys Leu Val His Phe Leu Phe
 35 40 45
 Tyr Ile Asn Leu Tyr Gly Ser Ile Leu Leu Leu Thr Cys Ile Ser Val
 50 55 60
 His Gln Phe Leu Gly Val Cys His Pro Leu Cys Ser Leu Pro Tyr Arg
 65 70 75 80
 Thr Arg Arg His Ala Trp Leu Gly Thr Ser Thr Thr Trp Ala Leu Val
 85 90 95
 Val Leu Gln Leu Leu Pro Thr Leu Ala Phe Ser His Thr Asp Tyr Ile
 100 105 110
 Asn Gly Gln Met Ile Trp Tyr Asp Met Thr Ser Gln Glu Asn Phe Asp
 115 120 125
 Arg Leu Phe Ala Tyr Gly Ile Val Leu Thr Leu Ser Gly Phe Leu Ser
 130 135 140
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 145 150 155 160
 Gln Ala Arg Gly Glu Pro His Glu Asp Arg
 165 170

<210> 15
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 <222> (431)..(461)
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ccaccagacg gagagtaggt ggccacaagc gacacccatg atcttaacag gcgcgacgaa 300
gcccgcgacg gcctcataga acgcgtacac ctgcacgtgc cagcgctgca ggagcgcgaa 360
gatccagtgg cagcgacgca tccccggcca ggctcgggcg gagagtggcg cgcttggtg 420
cagagacgtt nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nagtactagc gcaccacaaa 480
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cagcaggtgg gccgaggcgc cccgcccgga tgccctgcagc agctgcagga agcggcacgc 660
caggtccccg gtggccgcgc ggggctcgcc cagcagttcc caggccagct gtgacagcgc 720
cgtgcccccg cagcgtaca ggtccgccag ggccagctgc accagcagga agtccatctt 780
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<210> 16
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 <213> H.Sapiens

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 <223> Xaa is unknown

<220>
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 <222> (144)..(154)
 <223> Xaa is Unknown

<400> 16

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Gly Asn Thr Thr Val Leu Cys Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20          25          30
Xaa Xaa Xaa Lys Arg Arg Lys Met Asp Phe Leu Leu Val Gln Leu Ala
35          40          45
Leu Ala Asp Leu Tyr Ala Cys Gly Gly Thr Ala Leu Ser Gln Leu Ala

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50	55	60
Trp Glu Leu Leu Gly 65	Glu Pro Arg Ala Ala Thr 70	Gly Asp Leu Ala Cys 75 80
Arg Phe Leu Gln 85	Leu Leu Gln Ala Ser Gly 90	Arg Gly Ala Ser Ala His 95
Leu Val Val Leu 100	Ile Ala Leu Glu Arg 105	Arg Arg Ala Val Arg Leu Pro 110
His Gly Arg Pro Leu Pro Ala Arg 115	Ala Leu Ala Ala Leu Gly Trp Leu 120 125	
Leu Ala Leu Leu Leu Ala Arg Gly Ser Gly Phe 130	Val Val Arg Tyr Xaa 135 140	
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr 145	Ser Leu Gln Pro Gly 150 155	
Ala Pro Leu Ser Ala Arg Ala Trp Pro Gly Met Arg Arg Cys His Trp 165	170 175	
Ile Phe Ala Leu Leu Gln Arg Trp His Val Gln Val Tyr Ala Phe Tyr 180	185 190	
Glu Ala Val Ala Gly Phe Val Ala Pro Val Lys Ile Met Gly Val Ala 195	200 205	
Cys Gly His Leu Leu Ser Val Trp Trp Arg His Arg Leu Lys Ala Pro 210	215 220	
Ala Gly Ala Ala Ala Trp Ser Ala Ser Pro Gly Gly Ala Arg Ala Pro 225	230 235 240	
Ser Ala Met Pro Arg Ala Lys Val Gln Ser Leu Lys Met Ser Gln Leu 245	250 255	
Leu Gly Leu Leu Phe Val Gly Cys Glu Leu Pro Phe Ala Asp Arg Leu 260	265 270	
Glu Ala Ala Trp Ser Ser Gly Pro Ala Gly Glu Trp Glu Gly Glu Ala 275	280 285	
Leu Ser Ala Cys Cys Ala Trp Trp 290	295	

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 <212> DNA
 <213> H.Sapiens

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ggggaggagg tagaatagga aggaggtgac ctggatgatg aaattgtaga tccacatggg	180

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cttgatgacc gtacaggtgg ccgaacctgg gaccagggac ccattgggga agtagtgga 240
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gccgaggatc ctgagggccc ggcgccgggt gctctgcagt ttggcgcgga acgggtgtag 360
gatggccacg tagcgctcca cgctgacggt ggtgatgctg aggatggagg cgaagcacac 420
ggtctcaaag agggccgtct tgaagtagca gcccacgggc ccgaacaaga :agggtagtt 480
gcgccacatc tcatagacct ccaggggcat tccaaggagc aggaccagga ggtcagagac 540
cgccaggctg aagaggtagt agttggtggg cgtcttcata gcctggtgct gcagaatcac 600
caggcacacc aggacattgc caatgacccc caccacaaaa attggcacat acaccacaga 660
cacggggagg aagaagtggc tgcgccgagg tccgcagagg aaggccagat actcctcggt 720
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ctgaagtttt tccatccctg a 801

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<210> 18
 <211> 249
 <212> PRT
 <213> H.Sapiens

<400> 18

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Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys
1          5          10          15
Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu
20        25        30
Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser
35        40        45
Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu
50        55        60
Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Asn Thr
65        70        75        80
Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu
85        90        95
Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu
100       105       110
Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val
115       120       125
Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr
130       135       140
Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg
145       150       155       160

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Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe
 165 170 175

Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro
 180 185 190

Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro
 195 200 205

Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr
 210 215 220

Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu
 225 230 235 240

Arg Val Ser Ile Ala Gly Val Ala Gly
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<210> 19
 <211> 222
 <212> DNA
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 atgcggaaga aagcaaagtt ttccctcaga gagaatccag tg 222

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 <211> 73
 <212> PRT
 <213> H.Sapiens

<400> 20

Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile Gly Phe Ser Asn Ser
 1 5 10 15

Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn Glu Asn Phe Lys Lys
 20 25 30

Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val Asn Lys Thr Phe Ser
 35 40 45

Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr Met Met Arg Lys Lys
 50 55 60

Ala Lys Phe Ser Leu Arg Glu Asn Pro
 65 70

<210> 21
 <211> 447
 <212> DNA

<213> H.Sapiens

<400> 21

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catggcactc acaaatttgc agaagggcag cccaaacatc caagtcttct tgatgaggta      180
ggtcaagcga aatggcactg tcagcagaaa aacgctgtgg accaccacca agttaatgac      240
cgccatggtg gtcactgacc ggggtgttcat tttcaccagg aggaaaagaa tggaaatgac      300
accaccagc ccgccaataa gcactatgaa gtagaggctg attaagtggg gtgtcactat      360
aggatcgcaa gaggaattcc tggaggtatt gtggccaggc atacttggga agtcacctgg      420
aggagaaaaa gcaccagagt aactgac                                          447

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<210> 22

<211> 149

<212> PRT

<213> H.Sapiens

<400> 22

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Val Ser Tyr Ser Gly Ala Phe Ser Pro Pro Gly Asp Phe Pro Ser Met
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Pro Gly His Asn Thr Ser Arg Asn Ser Ser Cys Asp Pro Ile Val Thr
20          25          30
Pro His Leu Ile Ser Leu Tyr Phe Ile Val Leu Ile Gly Gly Leu Val
35          40          45
Gly Val Ile Ser Ile Leu Phe Leu Leu Val Lys Met Asn Thr Arg Ser
50          55          60
Val Thr Thr Met Ala Val Ile Asn Leu Val Val Val His Ser Val Phe
65          70          75          80
Leu Leu Thr Val Pro Phe Arg Leu Thr Tyr Leu Ile Lys Lys Thr Trp
85          90          95
Met Phe Gly Leu Pro Phe Cys Lys Phe Val Ser Ala Met Leu His Ile
100         105         110
His Met Tyr Leu Thr Val Pro Ile Leu Cys Gly Asp Pro Gly His Gln
115         120         125
Ile Pro His Leu Leu Gln Val Gln Arg Gln Ser Gly Ile Leu Gln Lys
130         135         140
Thr Ala Cys Cys Gly
145

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<210> 23

<211> 222

<212> DNA
<213> H.Sapiens

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agcgaacacg gtcagcagca ccagtccatt gcagagcacg gagagcaaca cgatggccca 180
cacggccagg cggatgcccc agctttcaaa gaggtactca ca 222

<210> 24
<211> 74
<212> PRT
<213> H.Sapiens

<400> 24
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1 5 10 15
Ile Val Leu Leu Ser Val Leu Cys Asn Gly Leu Val Leu Leu Thr Val
20 25 30
Phe Ala Gly Gly Pro Ala Pro Leu Pro Pro Val Lys Phe Val Val Gly
35 40 45
Ala Ile Ala Gly Ala Asn Thr Leu Thr Gly Ile Ser Cys Gly Leu Leu
50 55 60
Ala Ser Val Asp Ala Leu Thr Leu Val Ser
65 70

<210> 25
<211> 246
<212> DNA
<213> H.Sapiens

<400> 25
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tgctgcggac gccactcctg cggcagagac ccgagtggct ccagcagtc ggcgagcgcg 120
gctgaggctt ccgggggcct gcgcgctgc ctgcccccg gccttgatgg gagcttcagc 180
ggctcggagc gtcacgcgc ccagcgcgac gggctggaca ccagcggctc cacaggcagc 240
cccggt 246

<210> 26
<211> 82
<212> PRT
<213> H.Sapiens

<400> 26

Asn Pro Ile Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg His Ala Leu
 1 5 10 15
 Leu Arg Leu Val Cys Cys Gly Arg His Ser Cys Gly Arg Asp Pro Ser
 20 25 30
 Gly Ser Gln Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly Gly Leu Arg
 35 40 45
 Arg Cys Leu Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly Ser Glu Arg
 50 55 60
 Ser Ser Pro Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser Thr Gly Ser
 65 70 75 80
 Pro Gly

<210> 27
 <211> 420
 <212> DNA
 <213> H.Sapiens
 <220>
 <221> misc_feature
 <222> (81)..(106)
 <223> n is any nucleic acid

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 cgcgatgcgg gcgtacatga ccacgatgag cgccagcggc gccaggtaga tgtgagagaa 180
 gagcacagtg gtgtagaccc tgcgcatgcc cttctcgggc caggcctccc agcaggagta 240
 gagagggtag gagcggttgc gggcggtccac catgaagtgg tgctcctcac gggtgacggt 300
 cagcgtgacg gccgagggac acatgatgag cagcgccagg gccagatga cggcgatggt 360
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<210> 28
 <211> 139
 <212> PRT
 <213> H.Sapiens
 <220>
 <221> UNSURE
 <222> (104)..(113)
 <223> Xaa is Unknown

<400> 28
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20	25	30	
Cys Pro Ser Ala	Val Thr Leu Thr	Val Thr Arg Glu	Glu His His Phe
35	40	45	
Met Val Asp Ala	Arg Asn Arg Ser	Tyr Pro Leu Tyr	Ser Cys Trp Glu
50	55	60	
Ala Trp Pro Glu	Lys Gly Met Arg	Arg Val Tyr Thr	Thr Val Leu Phe
65	70	75	80
Ser His Ile Tyr	Leu Ala Pro Leu	Ala Leu Ile Val	Val Met Tyr Ala
85	90	95	
Arg Ile Ala Arg	Lys Leu Cys Xaa	Xaa Xaa Xaa Xaa	Xaa Xaa Xaa
100	105	110	
Xaa Glu Ala Ala	Asp Pro Arg Ala	Ser Arg Arg Arg	Ala Arg Val Val
115	120	125	
His Met Leu Val	Met Val Ala Leu	Phe Phe Thr	
130	135		

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 <211> 318
 <212> DNA
 <213> H.Sapiens

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 cacagcacag gctttcacia aactcgcca gtagcaggcc acgatgtagg gtgaccagag 180
 gagcagaaaag agcagtgtga tcgcgtagaa catgcggccc agctgctttt cacccttgac 240
 ctctccatg ccagtagcc gccggctggc tgcattgcca ttctgccgga taccagcag 300
 ggttggtggc atgggccc 318

<210> 30
 <211> 106
 <212> PRT
 <213> H.Sapiens

<400> 30

Gly Pro Met Pro	Pro Thr Leu Leu	Gly Ile Arg Gln	Asn Gly His Ala
1	5	10	15
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20	25	30	
Leu Gly Arg Met	Phe Tyr Ala Ile	Thr Leu Leu Phe	Leu Leu Leu Trp

35 40 45
 Ser Pro Tyr Ile Val Ala Cys Tyr Trp Arg Val Phe Val Lys Ala Cys
 50 55 60
 Ala Val Pro His Arg Tyr Leu Ala Thr Ala Val Trp Met Ser Phe Ala
 65 70 75 80
 Gln Ala Ala Val Asn Pro Ile Val Cys Phe Leu Leu Asn Lys Asp Leu
 85 90 95
 Lys Lys Cys Leu Arg Thr His Ala Pro Cys
 100 105

<210> 31
 <211> 354
 <212> DNA
 <213> H.Sapiens

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 ctggtgcctt tccacagcaa tgcaggtcat agtgaggatt tctgtcacia cagcggtaga 180
 ctggacaaat ggcaccatct tgcaaatgaa agcacctgca gtaaggaaat aggataaatc 240
 atacatcaaa acaaaaagaa taaaggtttc atctgtgtct ttgtaattat cactatcagt 300
 ccattctgag cctctgcaa aaagtttgat aattgtaatt actctgtaga caca 354

<210> 32
 <211> 117
 <212> PRT
 <213> H.Sapiens

<400> 32

Val Tyr Arg Val Ile Thr Ile Ile Lys Leu Phe Gly Arg Gly Ser Glu
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 Trp Thr Asp Ser Asp Asn Tyr Lys Asp Thr Asp Glu Thr Phe Ile Leu
 20 25 30
 Phe Val Leu Met Tyr Asp Leu Ser Tyr Phe Leu Thr Ala Gly Ala Phe
 35 40 45
 Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala Val Val Thr Glu
 50 55 60
 Ile Leu Thr Met Thr Cys Ile Ala Val Glu Arg His Gln Gly Leu Val
 65 70 75 80
 His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg Arg Ala Phe Thr
 85 90 95
 Met Leu Gly Glu Ala Thr Gly Cys Ala Asn Gly Ser Val Asn Asp Ile

100 105 110

Leu His Tyr Arg Ile
115

<210> 33
<211> 621
<212> DNA
<213> H.Sapiens

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agtgttgatc atgctgttgc tcatggcgat gcactcgacg atgtagaagg cagtgaggta 120
gtgcttctcc ttcacaaaca cgggtggggaa gaagtcgctc acgatgggtga agccgtagaa 180
gggcgcccag catagcacgt aggcgggtgag gatgcacatg agcaccagga ccgtcttcct 240
gcggcagcgc agcctcttgc ggatctgctc tgtctggaat ccagggaccg ccttgaacca 300
gagctcccgg gagatcctgg catagcacag ggtcatgggtg accacggggc ccacgaattc 360
tatgccaaag ataaagagga agtaggactt gtagtagagc tgctggtcca caggccagat 420
ctggccgcag aagatctttt cctgggtctt gacaatgacg aggaccgtct cgggtggtgaa 480
gtaggcggaa gggatggcga tcaggatgga caccgtccac accaaggcaa tcaggccagt 540
ggctgttttg cacttcattc gtggtctcag cggatggaca atagccagat acctagggca 600
agaacacaag tggaggcagc c 621

<210> 34
<211> 207
<212> PRT
<213> H.Sapiens

<400> 34

Gly Cys Leu His Leu Cys Ser Cys Pro Arg Tyr Leu Ala Ile Val His
1 5 10 15
Pro Leu Arg Pro Arg Met Lys Cys Gln Thr Ala Thr Gly Leu Ile Ala
20 25 30
Leu Val Trp Thr Val Ser Ile Leu Ile Ala Ile Pro Ser Ala Tyr Phe
35 40 45
Thr Thr Glu Thr Val Leu Val Ile Val Lys Ser Gln Glu Lys Ile Phe
50 55 60
Cys Gly Gln Ile Trp Pro Val Asp Gln Gln Leu Tyr Tyr Lys Ser Tyr
65 70 75 80
Phe Leu Phe Ile Phe Gly Ile Glu Phe Val Gly Pro Val Val Thr Met
85 90 95

Thr Leu Cys Tyr Ala Arg Ile Ser Arg Glu Leu Trp Phe Lys Ala Val
 100 105 110
 Pro Gly Phe Gln Thr Glu Gln Ile Arg Lys Arg Leu Arg Cys Arg Arg
 115 120 125
 Lys Thr Val Leu Val Leu Met Cys Ile Leu Thr Ala Tyr Val Leu Cys
 130 135 140
 Trp Ala Pro Phe Tyr Gly Phe Thr Ile Val Arg Asp Phe Phe Pro Thr
 145 150 155 160
 Val Phe Val Lys Glu Lys His Tyr Leu Thr Ala Phe Tyr Ile Val Glu
 165 170 175
 Cys Ile Ala Met Ser Asn Ser Met Ile Asn Thr Leu Cys Phe Val Thr
 180 185 190
 Val Lys Asn Asp Thr Val Lys Tyr Phe Lys Lys Ile Met Leu Leu
 195 200 205

<210> 35
 <211> 483
 <212> DNA
 <213> H.Sapiens

<400> 35
 cagccacact gcagtgatga aatcaaatgt ccaacaccaa ccatagtcac cattactaac 60
 taagaagcca caaaacttcc cttccagggt gttcagcagc agggacaggg cccagggcag 120
 ggcacacatg acagttgaca ggtttcttgg gcagcagcag cagtaccaga taggccgcag 180
 gacagacagg cagcactcag tactgatggc actcagcatg ctcaggccta caaggtaggc 240
 aaaggtcatc acgctggtga agaagctagg gaaattgatg gagatggaac agaagaagtt 300
 actgaggtac accaggcaat ttataatctg gaagcagagg aagaggaagt cggccccggc 360
 caggctgagg acgtagacag agaaggcggt cctgcgcagc cggaagccca ggagccagag 420
 cacaaacccg ttctctacca gcccgaccag ggcaatgaaa aggatcagga agaccgggat 480
 cag 483

<210> 36
 <211> 161
 <212> PRT
 <213> H.Sapiens

<400> 36

Leu Ile Pro Val Phe Leu Ile Leu Phe Ile Ala Leu Val Gly Leu Val
 1 5 10 15
 Gly Asn Gly Phe Val Leu Trp Leu Leu Gly Phe Arg Met Arg Arg Asn
 20 25 30

Ala Phe Ser Val Tyr Val Leu Ser Leu Ala Gly Ala Asp Phe Leu Phe
 35 40 45
 Leu Cys Phe Gln Ile Ile Asn Cys Leu Val Tyr Leu Ser Asn Phe Phe
 50 55 60
 Cys Ser Ile Ser Ile Asn Phe Pro Ser Phe Phe Thr Ser Val Met Thr
 65 70 75 80
 Phe Ala Tyr Leu Val Gly Leu Ser Met Leu Ser Ala Ile Ser Thr Glu
 85 90 95
 Cys Cys Leu Ser Val Leu Arg Pro Ile Trp Tyr Cys Cys Cys Cys Pro
 100 105 110
 Arg Asn Leu Ser Thr Val Met Cys Ala Leu Pro Trp Ala Leu Ser Leu
 115 120 125
 Leu Leu Asn Thr Leu Glu Gly Lys Phe Cys Gly Phe Leu Val Ser Asn
 130 135 140
 Gly Asp Tyr Gly Trp Cys Trp Thr Phe Asp Phe Ile Thr Ala Val Trp
 145 150 155 160

Leu

<210> 37
 <211> 330
 <212> DNA
 <213> H.Sapiens

<400> 37
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 atcctttgct tgtccgttga ggctcctagtc tggagccaag tgacaaagac agagatcacc 120
 tatttacgcc atgtgtgcat tgtaacatt gcagccactt tgctgatggc agatgtgtgg 180
 ttcatgtgg cttcctttct tagtggccca ataacacacc acaagggatg tgtggcagcc 240
 acattttttg gtcattttct ttacctttct gtatttttct ggatgcttgc caaggcactc 300
 cttatcctct atggaatcat gattgttttc 330

<210> 38
 <211> 110
 <212> PRT
 <213> H.Sapiens

<400> 38
 Glu Ser Leu Ile Leu Thr Tyr Ile Thr Tyr Val Gly Leu Gly Ile Ser
 1 5 10 15
 Ile Cys Ser Leu Ile Leu Cys Leu Ser Val Glu Val Leu Val Trp Ser
 20 25 30

Gln Val Thr Lys Thr Glu Ile Thr Tyr Leu Arg His Val Cys Ile Val
 35 40 45
 Asn Ile Ala Ala Thr Leu Leu Met Ala Asp Val Trp Phe Ile Val Ala
 50 55 60
 Ser Phe Leu Ser Gly Pro Ile Thr His His Lys Gly Cys Val Ala Ala
 65 70 75 80
 Thr Phe Phe Gly His Phe Phe Tyr Leu Ser Val Phe Phe Trp Met Leu
 85 90 95
 Ala Lys Ala Leu Leu Ile Leu Tyr Gly Ile Met Ile Val Phe
 100 105 110

<210> 39
 <211> 628
 <212> DNA
 <213> H.Sapiens

<400> 39
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 ctttaaataa ggacagtaaa tcccatcacg cagggtggtg gggagaatca gagatgatac 180
 agctggtgat cacatctggt ttgtgttccc aggggcacca gactagggtt tctgagcatg 240
 gatccaaccg tcccagtctt cggtacaaaa ctgacaccaa tcaacggacg tgaggagact 300
 ccttgctaca atcagaccct gagcttcacg gtgctgacgt gcatcatttc ccttgctcga 360
 ctgacaggaa acgcggtagt gctctggctc ctgggctacc gcatgcgcag gaacgctgtc 420
 tccatctaca tcctcaacct ggccgcagca gacttctctt tcctcagctt ccagattata 480
 cgttcgccat tacgcctcat caatatcagc catctcatcc gcaaaatcct cgtttctgtg 540
 atgaccttct cctactttac aggctgagt atgctgagcg ccatcagcac cgagcgctgc 600
 ctgtctgttc tgtggcccat ctggtacc 628

<210> 40
 <211> 205
 <212> PRT
 <213> H.Sapiens

<400> 40

Leu Cys Gly Ser Arg Glu Met Ser Gly Phe Arg Val Asn Lys Asn Trp
 1 5 10 15
 Ile Ser Asn Trp Ile Gly Pro Pro Pro Leu Val Ser Asp Leu Leu Ser
 20 25 30
 Ala Ser Leu Cys Phe Ser Leu Leu Met Arg Thr Val Asn Pro Ile Arg
 35 40 45

Gln Gly Gly Gly Glu Asn Gln Arg Tyr Ser Trp Ser His Leu Val Cys
 50 55 60
 Val Pro Arg Gly Thr Arg Leu Gly Phe Leu Ser Met Asp Pro Thr Val
 65 70 75 80
 Pro Val Phe Gly Thr Lys Leu Thr Pro Ile Asn Gly Arg Glu Glu Thr
 85 90 95
 Pro Cys Tyr Asn Gln Thr Leu Ser Phe Thr Val Leu Thr Cys Ile Ile
 100 105 110
 Ser Leu Val Gly Leu Thr Gly Asn Ala Val Val Leu Trp Leu Leu Gly
 115 120 125
 Tyr Arg Met Arg Arg Asn Ala Val Ser Ile Tyr Ile Leu Asn Leu Ala
 130 135 140
 Ala Ala Asp Phe Leu Phe Leu Ser Phe Gln Ile Ile Arg Ser Pro Leu
 145 150 155 160
 Arg Leu Ile Asn Ile Ser His Leu Ile Arg Lys Ile Leu Val Ser Val
 165 170 175
 Met Thr Phe Pro Tyr Phe Thr Gly Leu Ser Met Leu Ser Ala Ile Ser
 180 185 190
 Thr Glu Arg Cys Leu Ser Val Leu Trp Pro Ile Trp Tyr
 195 200 205

<210> 41
 <211> 319
 <212> DNA
 <213> H.Sapiens

<400> 41
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 ctgcccttct ttgtcttgac gatcacagat cctttcatta attttacaac ccttgaagat 120
 ctgtacaatg tcttctcttg gctaggctat ttcaactctg ctttcaatcc cattttatat 180
 ggcatgcttt atccttggtt tcgcaaggca ttgaggtatga ttgtcacagg catgatcttc 240
 caccctgact cttccaccct aagcctgttt tctgcccattg cttaggctgt gttcatcatt 300
 caataggact cttttcttg 319

<210> 42
 <211> 103
 <212> PRT
 <213> H.Sapiens

<400> 42

Thr Glu Ser Lys Ala Thr Arg Thr Leu Gly Ile Val Met Gly Val Phe
 1 5 10 15

Val Leu Cys Trp Leu Pro Phe Phe Val Leu Thr Ile Thr Asp Pro Phe
 20 25 30
 Ile Asn Phe Thr Thr Leu Glu Asp Leu Tyr Asn Val Phe Leu Trp Leu
 35 40 45
 Gly Tyr Phe Asn Ser Ala Phe Asn Pro Ile Leu Tyr Gly Met Leu Tyr
 50 55 60
 Pro Trp Phe Arg Lys Ala Leu Arg Met Ile Val Thr Gly Met Ile Phe
 65 70 75 80
 His Pro Asp Ser Ser Thr Leu Ser Leu Phe Ser Ala His Ala Ala Val
 85 90 95
 Phe Ile Ile Gln Asp Ser Phe
 100

<210> 43
 <211> 515
 <212> DNA
 <213> H.Sapiens

<400> 43
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 gaatcagcaa atcttattca cttatcacta aatctaaaat atgtcaaaat acatgaagac 120
 aacaaatgct ttagaacaac tgttgaatgt attgtcctac aacttggcat atgatcatgc 180
 ttgcctctct atgtccaagt gtttattttt gcagttgacc ttaatttcaa gttagttttg 240
 aggtctctac agtaatgttt ttaatctgtc tctacttctt cagaaaataa attagttgtt 300
 gacgaatcag tccttaagac cttgccgctt acaataagtt ttattgcctt cccaaaccat 360
 tggtaaaaga aagcataaat caaggggttc atagctgaat tataataaac acaccaaact 420
 aaaatctcat aaacataagg aggagttata aaattcatat aagcatcaat cactgcatca 480
 acgaggtatg gtagccaaga gacaagaaat gctgc 515

<210> 44
 <211> 148
 <212> PRT
 <213> H.Sapiens

<400> 44

Leu His Gln Arg Gly Met Val Ala Lys Arg Gln Glu Met Leu Ala Ala
 1 5 10 15
 Phe Leu Val Ser Trp Leu Pro Tyr Leu Val Asp Ala Val Ile Asp Ala
 20 25 30
 Tyr Met Asn Phe Ile Thr Pro Pro Tyr Val Tyr Glu Ile Leu Val Trp
 35 40 45

Cys Val Tyr Tyr Asn Ser Ala Met Asn Pro Leu Ile Tyr Ala Phe Phe
 50 55 60
 Tyr Gln Trp Phe Gly Lys Ala Ile Lys Leu Ile Val Ser Gly Lys Val
 65 70 75 80
 Leu Arg Thr Asp Ser Ser Thr Thr Asn Leu Phe Ser Glu Glu Val Glu
 85 90 95
 Thr Asp Lys His Tyr Cys Arg Asp Leu Lys Thr Asn Leu Lys Leu Arg
 100 105 110
 Ser Thr Ala Lys Ile Asn Thr Trp Thr Arg Gly Lys His Asp His Met
 115 120 125
 Pro Ser Cys Arg Thr Ile His Ser Thr Val Val Leu Lys His Leu Leu
 130 135 140

Ser Ser Cys Ile
145

<210> 45
 <211> 726
 <212> DNA
 <213> H.Sapiens

<400> 45
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 acaaactttc tgattgcgtc gctggcctgt gctgacttct tgggtgggagt cactgtgatg 180
 cccttcagca cagtgaggtc tgtggagagc tgtttggtact ttggggacag ttactgtaaa 240
 ttccatacat gttttgacac atctttctgt tttgcttctt tatttcattt atgctgtatc 300
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 tcagtttcag ggatatgcat tggtctttcc tgggtctttt ctgtcacata cagcttttgc 420
 atctttttaca cgggagccaa cgaagaagga attgaggaat tagtagttgc tctaacctgt 480
 gtaggaggct gccaggctcc actgaatcaa aactgggtcc tactttgttt tcttctattc 540
 tttataccca atgtcgccat ggtgtttata tacagtaaga ttttttgggt ggccaagcat 600
 caggctagga agatagaaag tacagccagc caagctcagt ccttctcaga gagttacaag 660
 gaaagagtag caaaaagaga gagaaaggct gccaaaacct tgggaattgc tatggcagca 720
 tttctt 726

<210> 46
 <211> 241
 <212> PRT
 <213> H.Sapiens

<400> . 46

Leu Glu Arg Gly Pro Arg Ser Ile Leu Tyr Ala Val Leu Gly Phe Gly
 1 5 10 15
 Ala Val Leu Ala Ala Phe Gly Asn Leu Leu Val Met Ile Ala Ile Leu
 20 25 30
 His Phe Gln Leu His Thr Pro Thr Asn Phe Leu Ile Ala Ser Leu Ala
 35 40 45
 Cys Ala Asp Phe Leu Val Gly Val Thr Val Met Pro Phe Ser Thr Val
 50 55 60
 Arg Ser Val Glu Ser Cys Trp Tyr Phe Gly Asp Ser Tyr Cys Lys Phe
 65 70 75 80
 His Thr Cys Phe Asp Thr Ser Phe Cys Phe Ala Ser Leu Phe His Leu
 85 90 95
 Cys Cys Ile Ser Val Asp Arg Tyr Ile Ala Val Thr Asp Pro Leu Thr
 100 105 110
 Tyr Pro Thr Lys Phe Thr Val Ser Val Ser Gly Ile Cys Ile Val Leu
 115 120 125
 Ser Trp Phe Phe Ser Val Thr Tyr Ser Phe Ser Ile Phe Tyr Thr Gly
 130 135 140
 Ala Asn Glu Glu Gly Ile Glu Glu Leu Val Val Ala Leu Thr Cys Val
 145 150 155 160
 Gly Gly Cys Gln Ala Pro Leu Asn Gln Asn Trp Val Leu Leu Cys Phe
 165 170 175
 Leu Leu Phe Phe Ile Pro Asn Val Ala Met Val Phe Ile Tyr Ser Lys
 180 185 190
 Ile Phe Leu Val Ala Lys His Gln Ala Arg Lys Ile Glu Ser Thr Ala
 195 200 205
 Ser Gln Ala Gln Ser Phe Ser Glu Ser Tyr Lys Glu Arg Val Ala Lys
 210 215 220
 Arg Glu Arg Lys Ala Ala Lys Thr Leu Gly Ile Ala Met Ala Ala Phe
 225 230 235 240

Leu

<210> 47
 <211> 660
 <212> DNA
 <213> H.Sapiens

<400> 47
 aaccaggtgg ccttactcct aagacccttg gccttgtcta tggcctttat caacagctgt 60

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ctcaatccag ttctctatgt cttcattggg catgacttct gggagcactt gctccactcc 120
ctgctagctg ccttagaacg ggcacttagc gaggagccag atagtgcctg aatcccagct 180
cccaggcaga tgagtccttt ataacatgac ccaatttcct actccatttt ccaccactc 240
aatcctcttc ccaaacagct ctaccataat ccaacatcca acagaattta agagaataaa 300
ccacaacttt taa'tgagct ctatgtgcta ggtcatgttt tagaatacaa ccttaagtgc 360
ctggaagatg gaggcaagaa acaaacaagg tctcattctt tagaggaaga cagttcacca 420
agactcaaac agaaaaaaag atagttatct tgtgacaaaa caagtcataa aattgggtca 480
ggacctgcag caatgacttt atgctagaat ccagagcact agcaggaaac tgcttaaatt 540
ttacttaatc aaagtcaagt ttggacatac atgtcaggta aaacctagca gagatgagct 600
accttgattt taaaacttca agggatagct caatgtcatc aagatccttt tgatgacttg 660

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<210> 48
<211> 211
<212> PRT
<213> H.Sapiens
<400> 48

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Asn Gln Val Ala Leu Leu Leu Arg Pro Leu Ala Leu Ser Met Ala Phe
1          5          10          15
Ile Asn Ser Cys Leu Asn Pro Val Leu Tyr Val Phe Ile Gly His Asp
20        25        30
Phe Trp Glu His Leu Leu His Ser Leu Leu Ala Ala Leu Glu Arg Ala
35        40        45
Leu Ser Glu Glu Pro Asp Ser Ala Ile Pro Ala Pro Arg Gln Met Ser
50        55        60
Pro Leu His Asp Pro Ile Ser Tyr Ser Ile Phe Pro Pro Leu Asn Pro
65        70        75        80
Leu Pro Lys Gln Leu Tyr His Asn Pro Thr Ser Asn Arg Ile Glu Asn
85        90        95
Lys Pro Gln Leu Leu Ser Glu Leu Tyr Val Leu Gly His Val Leu Glu
100       105       110
Tyr Asn Leu Lys Cys Leu Glu Asp Gly Gly Lys Lys Gln Thr Arg Ser
115       120       125
His Ser Leu Glu Glu Asp Ser Ser Pro Arg Leu Lys Gln Lys Lys Arg
130       135       140
Leu Ser Cys Asp Lys Thr Ser His Lys Ile Gly Ser Gly Pro Ala Ala
145       150       155       160
Met Thr Leu Cys Asn Pro Glu His Gln Glu Thr Ala Ile Leu Leu Asn

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165 170 175

Gln Ser Gln Val Trp Thr Tyr Met Ser Gly Lys Thr Gln Arg Ala Thr
 180 185 190

Leu Ile Leu Lys Leu Gln Gly Ile Ala Gln Cys His Gln Asp Pro Phe
 195 200 205

Asp Asp Leu
 210

<210> 49
 <211> 465
 <212> DNA
 <213> H.Sapiens

<400> 49
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 agcggaggcg cgcggtgggc ctggccgagg tggctctgct ggcctttgtc acctgcttcg 120
 cccccaacaa ctctgtgtc ctggcgaca tctgagccg cctgtttctac ggcaagagct 180
 actaccacgt gtacaagctc acgctgtgtc tcagctgcct caacaactgt ctggaccctg 240
 ttgtttatta ctttgcgtcc cgggaattcc agctgcgcct gcgggaatat ttgggctgcc 300
 gccgggtgcc cagagacacc ctggacacgc gccgcgagag cctctttctcc gccaggacca 360
 cgtccgtgag ctccgaggcc ggtgcgcacc ctgaagggat ggaggagacc accaggcccg 420
 gcctccagag gcaggagagt gtgttctgag tcccgggggc gcagc 465

<210> 50
 <211> 160
 <212> PRT
 <213> H.Sapiens

<400> 50

Leu Phe Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu Glu Ala His
 1 5 10 15

Gly Arg Glu Gln Arg Arg Arg Ala Val Gly Leu Ala Ala Val Val Leu
 20 25 30

Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val Leu Leu Ala
 35 40 45

His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr His Val Tyr
 50 55 60

Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu Asp Pro Phe
 65 70 75 80

Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu Arg Glu Tyr
 85 90 95

Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr Arg Arg Glu
 100 105 110

Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu Ala Gly Ala
 115 120 125

His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu Gln Arg Gln
 130 135 140

Glu Ser Val Phe Val Pro Gly Ala Gln Ala Ala Pro Pro Gly Leu Arg
 145 150 155 160

<210> 51
 <211> 603
 <212> DNA
 <213> H.Sapiens

<400> 51
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 ggggggctgt cttccactac ttcctgctct gtgccttcac ctggatgggc cttgaagcct 540
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 agc 603

<210> 52
 <211> 198
 <212> PRT
 <213> H.Sapiens

<400> 52

Glu Thr Tyr Ser Ala Leu Tyr Pro Thr Phe Asn Ser Leu Cys Tyr Ser
 1 5 10 15

Pro Ala Ser Phe Ser Gly Leu Ile Phe Pro Ile Ile Leu Pro His Ile
 20 25 30

Asp Gln Gly Met Arg Leu Ala Gly Ser Gly Thr His Arg Ala Pro Trp
 35 40 45

Ala Met Arg Gly Ser Trp Thr Thr Ser Gly His Ser His Ser Gly Cys
 50 55 60

Asp His Phe Leu Trp His Pro Gly Glu Tyr Val Phe Phe Ser Ala Gly
1 5 10 15

Ala Met Lys Ile Arg Asn Asn Pro Val Phe Phe Val Ile Ile Asn Lys
20 25 30

Asp Lys Ile Ser Pro Tyr Val Asn Thr Ser Val Met Ser Ser Asn Ser
 35 40 45
 Ser Leu Leu Val Ala Val Gln Leu Cys Tyr Ala Asn Val Asn Gly Ser
 50 55 60
 Cys Val Lys Ile Pro Phe Ser Pro Gly Ser Arg Val Ile Leu Tyr Ile
 65 70 75 80
 Val Phe Gly Phe Gly Ala Val Leu Ala Val Phe Gly Asn Leu Leu Val
 85 90 95
 Met Ile Ser Ile Leu His Phe Lys Gln Leu His Ser Pro Thr Asn
 100 105 110

<210> 55
 <211> 586
 <212> DNA
 <213> H.Sapiens

<400> 55
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 tatcctgaac ttcgtctatc caactgctta tatatgttca gaaaacaaat tcatgggttc 180
 tgaactgttc tttaaaacct gaccagttac aataactttt attgctttcc taaaccatgg 240
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<210> 56
 <211> 190
 <212> PRT
 <213> H.Sapiens

<400> 56
 Leu Thr Asp Phe Leu Ser Phe Phe Ile Pro Thr Phe Ile Met Ile Ile
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 Leu Tyr Gly Asn Ile Phe Leu Val Ala Arg Arg Gln Ala Lys Lys Ile
 20 25 30
 Glu Asn Thr Gly Ser Lys Thr Glu Ser Ser Ser Glu Ser Tyr Lys Ala
 35 40 45

Arg Val Ala Arg Arg Glu Arg Lys Ala Ala Lys Thr Leu Gly Val Thr
 50 55 60
 Val Val Ala Phe Met Ile Ser Trp Leu Pro Tyr Ser Ile Asp Ser Leu
 65 70 75 80
 Ile Asp Ala Phe Met Gly Phe Ile Thr Pro Ala Cys Ile Tyr Glu Ile
 85 90 95
 Cys Cys Trp Cys Ala Tyr Tyr Asn Ser Ala Met Asn Pro Leu Ile Tyr
 100 105 110
 Ala Leu Phe Tyr Pro Trp Phe Arg Lys Ala Ile Lys Val Ile Val Thr
 115 120 125
 Gly Gln Val Leu Lys Asn Ser Ser Ala Thr Met Asn Leu Phe Ser Glu
 130 135 140
 His Ile Ala Val Gly Thr Lys Phe Arg Ile Pro Leu Lys Leu Pro Ser
 145 150 155 160
 Glu Met Ser Phe Lys Ser Ser Lys Thr Met Asn Glu Gln Ile Asn Cys
 165 170 175
 Ser Ser Asn Lys Gln Ile Asn Val Phe Gln Ser Cys Asp Val
 180 185 190

<210> 57
 <211> 976
 <212> DNA
 <213> H.Sapiens

<400> 57
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 ctgtctacgt cctcagcctg gccggggccg acttctctt cctctgcttc cagattataa 180
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 tcatcactgc agcgtggctg atttttttat tcatggttct ctgtgggtcc agtctggccc 540
 tgctggtcag gatcctctgt ggctccaggg gtctgccact gaccaggctg tacctgacca 600
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 taatattatg gatctggaag gattctgatg tcttattttg tcatattcat ccagtttcag 720
 ttgtcctgtc atctcttaac agcagtgcc aacctatcat ttacttcttc gtgggctctt 780

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ttaggaagca gtggcggstg cagcaccoga tcctcaagct ggctctccag agggctctgc      840
aggacattgc tgaggtggat cacagtgaag gatgcttccg tcagggcacc cggagattca      900
aagaagcatt ctggtgtagg gatggacccc tctacttcca tcatatatat gtggctttga      960
gaggcaactt tgcccc                                          976

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<210> 58
<211> 324
<212> PRT
<213> H.Sapiens

<220>
<221> UNSURE
<222> (266)..(266)
<223> Xaa is Unknown

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<400> 58

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Cys Gly Lys Glu Thr Leu Ile Pro Val Phe Leu Ile Leu Phe Ile Ala
1          5          10          15
Leu Val Gly Leu Val Gly Asn Gly Phe Val Leu Trp Leu Leu Gly Phe
20          25          30
Arg Met Arg Arg Asn Ala Phe Ser Val Tyr Val Leu Ser Leu Ala Gly
35          40          45
Ala Asp Phe Leu Phe Leu Cys Phe Gln Ile Ile Asn Cys Leu Val Tyr
50          55          60
Leu Ser Asn Phe Phe Cys Ser Ile Ser Ile Asn Phe Pro Ser Phe Phe
65          70          75          80
Thr Thr Val Met Thr Cys Ala Tyr Leu Ala Gly Leu Ser Met Leu Ser
85          90          95
Thr Val Ser Thr Glu Arg Cys Leu Ser Val Leu Trp Pro Ile Trp Tyr
100         105         110
Arg Cys Arg Arg Pro Arg His Leu Ser Ala Val Val Cys Val Leu Leu
115         120         125
Trp Ala Leu Ser Leu Leu Leu Ser Ile Leu Glu Gly Lys Phe Cys Gly
130         135         140
Phe Leu Phe Ser Asp Gly Asp Ser Gly Trp Cys Gln Thr Phe Asp Phe
145         150         155         160
Ile Thr Ala Ala Trp Leu Ile Phe Leu Phe Met Val Leu Cys Gly Ser
165         170         175
Ser Leu Ala Leu Leu Val Arg Ile Leu Cys Gly Ser Arg Gly Leu Pro
180         185         190
Leu Thr Arg Leu Tyr Leu Thr Ile Leu Leu Thr Val Leu Val Ser Leu

```

195					200					205					
Leu	Cys	Gly	Leu	Pro	Phe	Gly	Ile	Gln	Trp	Phe	Leu	Ile	Leu	Trp	Ile
210						215					220				
Trp	Lys	Asp	Ser	Asp	Val	Leu	Phe	Cys	His	Ile	His	Pro	Val	Ser	Val
225					230					235					240
Val	Leu	Ser	Ser	Leu	Asn	Ser	Ser	Ala	Asn	Pro	Ile	Ile	Tyr	Phe	Phe
				245					250					255	
Val	Gly	Ser	Phe	Arg	Lys	Gln	Trp	Arg	Xaa	Gln	His	Pro	Ile	Leu	Lys
			260					265						270	
Leu	Ala	Leu	Gln	Arg	Ala	Leu	Gln	Asp	Ile	Ala	Glu	Val	Asp	His	Ser
		275					280					285			
Glu	Gly	Cys	Phe	Arg	Gln	Gly	Thr	Arg	Arg	Phe	Lys	Glu	Ala	Phe	Trp
	290					295					300				
Cys	Arg	Asp	Gly	Pro	Leu	Tyr	Phe	His	His	Ile	Tyr	Val	Ala	Leu	Arg
305					310					315					320
Gly Asn Phe Ala															

<210> 59
 <211> 578
 <212> DNA
 <213> H.Sapiens

<400> 59
 ctttgcatct cactgttgag cagacagcct gctgaaagtt gtcgctgacc accacatata 60
 gtaacagggt accaaagggtg ttcagagcag cataatgggtc tagaaacgat gtaagcttca 120
 tggatctgat tctcaatgga acaactgatt gaaagcaggc tgagattcga tcttgaatga 180
 ccctcaagat atggaagggt aaaaaacata cgtaaaatgc aaggagtagc agaattggta 240
 gccttcgtgc tttctgctta aggcagctgt cagtttgcag tccatgggtc aaagtgtgga 300
 taatcgtggt atagcaaagt gtcactatca ccaaggggag gcagaaagta cttgcagtca 360
 aaatcagggt gtaccactta atagtattga gttcatccga actggtgagg tcgagacagg 420
 ctgatctgtt ggtcctgttg gttgatgtga tcaagaaggt catcggaatg acagctacca 480
 gtgaaatgat ccacaccaca gcacaggcta caactgcaca tcgagttttg tgaatggaaa 540
 agcagctcat tgggtgaatg atcacacagt agcggaag 578

<210> 60
 <211> 192
 <212> PRT
 <213> H.Sapiens

<400> 60

Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe Ser Ile His
 1 5 10 15
 Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val Val Trp Ile Ile Ser
 20 25 30
 Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser Thr Asn Arg
 35 40 45
 Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Glu Leu Asn
 50 55 60
 Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Ser Thr Phe Cys Leu
 65 70 75 80
 Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr Leu
 85 90 95
 Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys Gln Lys Ala Arg Arg
 100 105 110
 Leu Thr Ile Leu Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro Phe
 115 120 125
 His Ile Leu Arg Val Ile Gln Asp Arg Ile Ser Ala Cys Phe Gln Ser
 130 135 140
 Val Val Pro Leu Arg Ile Arg Ser Met Lys Leu Thr Ser Phe Leu Asp
 145 150 155 160
 His Tyr Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val
 165 170 175
 Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys Lys
 180 185 190

<210> 61
 <211> 872
 <212> DNA
 <213> H.Sapiens

<400> 61
 gggagggctc gtagacacac taaccctacc ctttctgttt cttcctcacc tttcctttcc 60
 atctgtttct catggtctcc tgtctgtctc tctctctctc ccctctttct ctctcctcgc 120
 tctttctcat cccctccatt tctgtgtcaa tctcaatcca tttatatcgg tggccacttt 180
 tctatctctt tgttctatct ctctctctct ctctttccca ctttgtctct gcacgcctgt 240
 tgtgtttttc tgccctgtctc tctcttgccc tcatctctct gtctctctct tgccctcacc 300
 tctctgtctc tctgtgtctg tgtctccccc gctcattccc atttgacagt gcaatgtagc 360
 aggacaactc atggagcccc cccgggcccc tcgagtaccg gactggctga cccctagagg 420
 ttggcagtag cccctgaccc tcagtatggc caacactacc ggagagcctg aggaggtgag 480

```

cggcgctctg tccccaccgt ccgcatcagc ttatgtgaag ctggtactgc tgggactgat      540
tatgtgcgtg agcctggcgg gtaacgccat cttgtccctg ctggtgctca aggagcgggc      600
cctgcacaag gctccttact acttcctgct ggacctgtgc ctggccgatg gcatacgctc      660
tgccgtctgc tccccctttg tgctggcttc tgtgcgccac ggctcttcat ggaccttcag      720
tgcaactcagc tgcaagattg tggcctttat ggccgtgctc ttttgcttcc atgcggcctt      780
catgctgttc tgcacacagc tcacccgcta catggccatc gccaccacc gcttctacgc      840
caagcgcgatg acactctgga catgcgcggc tg                                     872

```

<210> 62
 <211> 143
 <212> PRT
 <213> H.Sapiens

<400> 62

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Met Ala Asn Thr Thr Gly Glu Pro Glu Glu Val Ser Gly Ala Leu Ser
1           5           10           15
Pro Pro Ser Ala Ser Ala Tyr Val Lys Leu Val Leu Leu Gly Leu Ile
          20          25          30
Met Cys Val Ser Leu Ala Gly Asn Ala Ile Leu Ser Leu Leu Val Leu
          35          40          45
Lys Glu Arg Ala Leu His Lys Ala Pro Tyr Tyr Phe Leu Leu Asp Leu
          50          55          60
Cys Leu Ala Asp Gly Ile Arg Ser Ala Val Cys Phe Pro Phe Val Leu
          65          70          75          80
Ala Ser Val Arg His Gly Ser Ser Trp Thr Phe Ser Ala Leu Ser Cys
          85          90          95
Lys Ile Val Ala Phe Met Ala Val Leu Phe Cys Phe His Ala Ala Phe
          100         105         110
Met Leu Phe Cys Ile Ser Val Thr Arg Tyr Met Ala Ile Ala His His
          115         120         125
Arg Phe Tyr Ala Lys Arg Met Thr Leu Trp Thr Cys Ala Ala Glu
          130         135         140

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<210> 63
 <211> 962
 <212> DNA
 <213> H.Sapiens

<400> 63

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aaaaattgct gtactgaact attgaatgga acttggaat aaagtcctt ccaaaataac      60
tattcttcaa cagagagtaa taggtaaatg ttttagaagt gagaggactc aaattgccaa      120

```

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tgatttactc ttttattttt cctcctaggt ttctgggata agtatgtgca aataaaaaat 180
aaacatgaga aggaactgta acctgattat ggatttggga aaaagataaa tcaacacaca 240
aagggaag taaactgatt gacagccctc aggaatgatg cccttttgcc acaatataat 300
taatatttcc tgtgtgaaaa acaactggtc aaatgatgtc cgtgcttccc tgtacagttt 360
aatggtgctc ataattctga ccacactcgt tggcaatctg atagttattg tttctatata 420
acacttcaaa caacttcata cccaacaaa ttggctcatt cattccatgg ccaactgtgga 480
ctttcttctg ggggtgtctgg tcatgcctta cagtatgggtg agatctgctg agcactgttg 540
gtattttgga gaagtcttct gtaaaattca cacaagcacc gacattatgc tgagctcagc 600
ctccattttc catttgtctt tcatctccat tgaccgctac tatgctgtgt gtgatccact 660
gagatataaa gccaaagatga atatcttggt tatttgtgtg atgatcttca ttagttggag 720
tgtccctgct gtttttgcac ttggaatgat ctttctggag ctaaacttca aaggcgctga 780
agagatatat tacaacatg ttcactgcag aggaggttgc tctgtcttct ttagcaaaat 840
atctggggta ctgaccttta tgacttcttt ttatatacct ggatctatta tgttatgtgt 900
ctattacaga atatatctta tcgctaaaga acaggcaaga ttaattagtg atgccaatca 960
ga 962

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<210> 64
 <211> 238
 <212> PRT
 <213> H.Sapiens

<400> 64

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Arg Glu Lys Thr Asp Gln Pro Ser Gly Met Met Pro Phe Cys His Asn
1          5          10          15
Ile Ile Asn Ile Ser Cys Val Lys Asn Asn Trp Ser Asn Asp Val Arg
20          25          30
Ala Ser Leu Tyr Ser Leu Met Val Leu Ile Ile Leu Thr Thr Leu Val
35          40          45
Gly Asn Leu Ile Val Ile Val Ser Ile Ser His Phe Lys Gln Leu His
50          55          60
Thr Pro Thr Asn Trp Leu Ile His Ser Met Ala Thr Val Asp Phe Leu
65          70          75          80
Leu Gly Cys Leu Val Met Pro Tyr Ser Met Val Arg Ser Ala Glu His
85          90          95
Cys Trp Tyr Phe Gly Glu Val Phe Cys Lys Ile His Thr Ser Thr Asp
100         105         110

```

Ile Met Leu Ser Ser Ala Ser Ile Phe His Leu Ser Phe Ile Ser Ile
 115 120 125

Asp Arg Tyr Tyr Ala Val Cys Asp Pro Leu Arg Tyr Lys Ala Lys Met
 130 135 140

Asn Ile Leu Val Ile Cys Val Met Ile Phe Ile Ser Trp Ser Val Pro
 145 150 155 160

Ala Val Phe Ala Phe Gly Met Ile Phe Leu Glu Leu Asn Phe Lys Gly
 165 170 175

Ala Glu Glu Ile Tyr Tyr Lys His Val His Cys Arg Gly Gly Cys Ser
 180 185 190

Val Phe Phe Ser Lys Ile Ser Gly Val Leu Thr Phe Met Thr Ser Phe
 195 200 205

Tyr Ile Pro Gly Ser Ile Met Leu Cys Val Tyr Tyr Arg Ile Tyr Leu
 210 215 220

Ile Ala Lys Glu Gln Ala Arg Leu Ile Ser Asp Ala Asn Gln
 225 230 235

<210> 65
 <211> 1018
 <212> DNA
 <213> H.Sapiens

<400> 65
 aacagtcccc ggtggaacct gggcatgtat attttgattg ttttatgcat actcctagtg 60
 aagaaccaat gtcttgctca gatagaagca agatactcag acttagtttc tctgtagctc 120
 ctgcttttta ttattcctgg ttggattgca ccactactca gtttctattt tataatactg 180
 attataaaac atgggagggg aataactttg tattggtttt tatggataat ttattatgtg 240
 tcctagactc tggccttgtc aaaagaagga cgtaagaagg cacgatgtat tatacttggg 300
 aatgatagaa gagactgacc tggatatttc acccggaaga gggaaaggat tttaactaca 360
 aatacaggaa tccagcagat ggcatcagag aacactataa aaaagaaacg atttgcaaca 420
 gccacctctc ttccaaaaca attccttact tctgtggtct gcaaggcggg tttttgaatg 480
 gaacagaaca tagtaatata ggaaaacaca atgatgagaa aagccagcaa gttcacacct 540
 gttggggaaa agcacacttt taacatctca ggcgtaaaag tcaacagtaa aattactgtg 600
 gtacagggttg agtatccctt acccaaatg tttgaaacca gaaatgtttt ggatttcgga 660
 tttcggaata ttacacatt cataatgata tatcttggaa atggttccca agtctaaaca 720
 caaaatttat ttatgtttca tatacacctt ataacacatag tctgaaagta atttgtaca 780
 atattttaaa taattttggg catgaaacaa agtttgcata cattgaacca tcagacagca 840
 aaagcttcag gtgtggaatt ttccacttgt ggcatcatgt tgatgctcaa aaagttccat 900

atttttagagc atttcaaatt ttggattttc aaattacaaa tgcttaacct gtacttagat 960
 gttaaataca gtgcctcttc cacgggcact ttcaggaagc attcttttat ataagccc 1018

<210> 66
 <211> 327
 <212> PRT
 <213> H.Sapiens

<400> 66

Tyr Ile Lys Glu Cys Phe Leu Lys Val Pro Val Glu Glu Ala Leu Tyr
 1 5 10 15
 Leu Thr Ser Lys Tyr Arg Leu Ser Ile Cys Asn Leu Lys Ile Gln Asn
 20 25 30
 Leu Lys Cys Ser Lys Ile Trp Asn Phe Leu Ser Ile Asn Met Met Pro
 35 40 45
 Gln Val Glu Asn Ser Thr Pro Glu Ala Phe Ala Val Trp Phe Asn Val
 50 55 60
 Cys Lys Leu Cys Phe Met Pro Lys Ile Ile Asn Ile Val Gln Asn Tyr
 65 70 75 80
 Phe Gln Thr Met Cys Ile Arg Cys Ile Asn Ile Asn Lys Phe Cys Val
 85 90 95
 Thr Trp Glu Pro Phe Pro Arg Tyr Ile Ile Met Asn Val Ile Phe Arg
 100 105 110
 Asn Pro Lys Ser Lys Thr Phe Leu Val Ser Asn Ile Leu Gly Lys Gly
 115 120 125
 Tyr Ser Thr Cys Thr Thr Val Ile Leu Leu Leu Thr Phe Thr Pro Glu
 130 135 140
 Met Leu Lys Val Cys Phe Ser Pro Thr Gly Val Asn Leu Leu Ala Phe
 145 150 155 160
 Leu Ile Ile Val Phe Ser Tyr Ile Thr Met Phe Cys Ser Ile Gln Lys
 165 170 175
 Thr Ala Leu Gln Thr Thr Glu Val Arg Asn Cys Phe Gly Arg Glu Val
 180 185 190
 Ala Val Ala Asn Arg Phe Phe Phe Ile Val Phe Ser Asp Ala Ile Cys
 195 200 205
 Trp Ile Pro Val Phe Val Val Lys Ile Leu Ser Leu Phe Arg Val Glu
 210 215 220
 Ile Pro Gly Gln Ser Leu Leu Ser Phe Pro Ser Ile Ile His Arg Ala
 225 230 235 240
 Phe Leu Arg Pro Ser Phe Asp Lys Ala Arg Val Asp Thr Ile Ile His

acaactccagc cacgatcgga tcccacagct cagccacagc tgaaccctac ggcccagcca 1140
 cagtcggatc ccacagccca gccacagctg aacctcatgg cccagccaca gtcagattct 1200
 gtggcccagc cacaggcaga cactaacgtc cagaccctg cacctgctgc c 1251

<210> 68
 <211> 417
 <212> PRT
 <213> H.Sapiens

<400> 68

Thr	Thr	Met	Glu	Ala	Asp	Leu	Gly	Ala	Thr	Gly	His	Arg	Pro	Arg	Thr
1				5					10					15	
Glu	Leu	Asp	Asp	Glu	Asp	Ser	Tyr	Pro	Gln	Gly	Gly	Trp	Asp	Thr	Val
			20					25					30		
Phe	Leu	Val	Ala	Leu	Leu	Leu	Leu	Gly	Leu	Pro	Ala	Asn	Gly	Leu	Met
		35					40					45			
Ala	Trp	Leu	Ala	Gly	Ser	Gln	Ala	Arg	His	Gly	Ala	Gly	Thr	Arg	Leu
	50					55					60				
Ala	Leu	Leu	Leu	Leu	Ser	Leu	Ala	Leu	Ser	Asp	Phe	Leu	Phe	Leu	Ala
65					70					75					80
Ala	Ala	Ala	Phe	Gln	Ile	Leu	Glu	Ile	Arg	His	Gly	Gly	His	Trp	Pro
				85					90					95	
Leu	Gly	Thr	Ala	Ala	Cys	Arg	Phe	Tyr	Tyr	Phe	Leu	Trp	Gly	Val	Ser
			100					105					110		
Tyr	Ser	Ser	Gly	Leu	Phe	Leu	Leu	Ala	Ala	Leu	Ser	Leu	Asp	Arg	Cys
		115					120					125			
Leu	Leu	Ala	Leu	Cys	Pro	His	Trp	Tyr	Pro	Gly	His	Arg	Pro	Val	Arg
	130					135					140				
Leu	Pro	Leu	Trp	Val	Cys	Ala	Gly	Val	Trp	Val	Leu	Ala	Thr	Leu	Phe
145					150					155					160
Ser	Val	Pro	Trp	Leu	Val	Phe	Pro	Glu	Ala	Ala	Val	Trp	Trp	Tyr	Asp
				165					170					175	
Leu	Val	Ile	Cys	Leu	Asp	Phe	Trp	Asp	Ser	Glu	Glu	Leu	Ser	Leu	Arg
			180					185					190		
Met	Leu	Glu	Val	Leu	Gly	Gly	Phe	Leu	Pro	Phe	Leu	Leu	Leu	Leu	Val
		195					200					205			
Cys	His	Val	Leu	Thr	Gln	Ala	Thr	Ala	Cys	Arg	Thr	Cys	His	Arg	Gln
	210					215					220				
Gln	Gln	Pro	Ala	Ala	Cys	Arg	Gly	Phe	Ala	Arg	Val	Ala	Arg	Thr	Ile
225					230					235					240

Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr Gln Leu Ala Gln Leu
 245 250 255
 Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu Leu Trp
 260 265 270
 Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser Cys Leu
 275 280 285
 Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr Leu Leu
 290 295 300
 Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu Cys Glu Glu Arg Pro
 305 310 315 320
 Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln Leu Asp Ser Glu Gly
 325 330 335
 Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln Ser Gln Met Asp Pro
 340 345 350
 Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln Pro Arg Ser Asp Pro
 355 360 365
 Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln Pro Gln Ser Asp Pro
 370 375 380
 Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln Pro Gln Ser Asp Ser
 385 390 395 400
 Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln Thr Pro Ala Pro Ala
 405 410 415

Ala

<210> 69
 <211> 659
 <212> DNA
 <213> H.Sapiens

<400> 69
 tacaggcctg agcatgctgg gctccatcag caccaagcac tgctgtcca tctgtggcc 60
 catctagtac cgctgccacc accccacaca cctgtcagca gtcgtgtgtc ctgctctggg 120
 ccctgtccct gctgcagagc atcctggaat ggatgttctg tggcttcctg tctagtgggtg 180
 ctgattctgt ttggtgtgaa acatcagatt tcatcacagt cacatggctg atttttttat 240
 gtgtggttct ctgcggttcc agcccgggtc tgctggtcag gatcctttgt ggatcccgga 300
 agatgccctt gaccaggctg tacatgacca tctgtctcag agtgctgggtc ttctctctct 360
 gtgacctgcc ctttggcatt cagtgattcc tatttttctg gatccacgtg gatttgtcac 420
 gttcgtctag tttccatttt cctgtccact cttaacagca gtgccaaccc cattattttac 480
 ttcttcatgg gctcctttag gcagcttcaa aacaggaaga ctctctagct ggttctccag 540

agggctctgc aggacacgcc tgagggtggaa gaaggcagat ggcggctttc tgaggaaacc 600
 ctggagctgt catgaagcag attggggcca tgaggaagag cctctgccct gtcagtcag 659

<210> 70
 <211> 213
 <212> PRT
 <213> H.Sapiens

<400> 70

Tyr Arg Pro Glu His Ala Gly Leu His Gln His Gln Ala Leu Pro Val
 1 5 10 15
 His Pro Val Ala His Leu Val Pro Leu Pro Pro Pro His Thr Pro Val
 20 25 30
 Ser Ser Arg Val Ser Cys Ser Gly Pro Cys Pro Cys Cys Arg Ala Ser
 35 40 45
 Trp Asn Gly Cys Ser Val Ala Ser Cys Leu Val Val Leu Ile Leu Phe
 50 55 60
 Gly Val Lys His Gln Ile Ser Ser Gln Ser His Gly Phe Phe Tyr Val
 65 70 75 80
 Trp Phe Ser Ala Gly Pro Ala Arg Phe Cys Trp Ser Gly Ser Phe Val
 85 90 95
 Asp Pro Gly Arg Cys Pro Pro Gly Cys Thr Pro Ser Cys Ser Glu Cys
 100 105 110
 Trp Ser Ser Ser Ser Val Thr Cys Pro Leu Ala Phe Ser Asp Ser Tyr
 115 120 125
 Phe Ser Gly Ser Thr Trp Ile Cys His Val Arg Leu Val Ser Ile Phe
 130 135 140
 Leu Ser Thr Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe Met
 145 150 155 160
 Gly Ser Phe Arg Gln Leu Gln Asn Arg Lys Thr Leu Leu Val Leu Gln
 165 170 175
 Arg Ala Leu Gln Asp Thr Pro Glu Val Glu Glu Gly Arg Trp Arg Leu
 180 185 190
 Ser Glu Glu Thr Leu Glu Leu Ser Ser Arg Leu Gly Pro Gly Arg Ala
 195 200 205
 Ser Ala Leu Ser Val
 210

<210> 71
 <211> 559
 <212> DNA
 <213> H.Sapiens

<400> 71
 atgccgaagg caggccgcag aagagaagag gaggacggtg aggaggatga gcccagggaa 60
 gccccgggggt gggggccgct gggggcctcg ctccacccgc agcagcagca taaggctggc 120
 cccacacatg gtgcaacaca gcagagccag cagcaccgct gccaccagcc acagcgtccg 180
 gcacaagtgg cggcgggct ccccgaagaa ctgggtgcag gcgccgctga gcagcaggtg 240
 cagcagcagg cagagggccc aggtgagggc gcacacacag gtggtcaggt ggcgtgggcg 300
 gcggcacagag taccaggctg ggaagagggc ggccaggcac tgctccacgc tgacggccgc 360
 caggagactc aggcccacga tgtagcagaa gaagcgcagc gttgccaggc tggctgcac 420
 gaagcccggg aagtccagcc ggccttgag caagtcgggg acgatggcca ccatgtggca 480
 gccaaaggaag atgagatccg cgcaggccac gtccaggagg tagatggcga aagggtttct 540
 gtagacattg gagctgagc 559

<210> 72
 <211> 211
 <212> PRT
 <213> H.Sapiens

<400> 72
 Leu Ser Ser Asn Val Tyr Arg Asn Pro Phe Ala Ile Tyr Leu Leu Asp
 1 5 10 15
 Val Ala Cys Ala Asp Leu Ile Phe Leu Gly Cys His Met Val Ala Ile
 20 25 30
 Val Pro Asp Leu Leu Gln Gly Arg Leu Asp Phe Pro Gly Phe Val Gln
 35 40 45
 Thr Ser Leu Ala Thr Leu Arg Phe Phe Cys Tyr Ile Val Gly Leu Ser
 50 55 60
 Leu Leu Ala Ala Val Ser Val Glu Gln Cys Leu Ala Ala Leu Phe Pro
 65 70 75 80
 Ala Trp Tyr Ser Cys Arg Arg Pro Arg His Leu Thr Thr Cys Val Cys
 85 90 95
 Ala Leu Thr Trp Ala Leu Cys Leu Leu Leu His Leu Thr Thr Cys Val
 100 105 110
 Cys Ala Leu Thr Trp Ala Leu Cys Leu Leu Leu His Leu Leu Leu Ser
 115 120 125
 Gly Ala Cys Thr Leu Leu Leu Ser Gly Ala Cys Thr Gln Phe Phe Gly
 130 135 140
 Glu Pro Ser Arg His Leu Cys Arg Thr Leu Trp Leu Val Ala Ala Val
 145 150 155 160

Leu Leu Ala Leu Leu Cys Cys Thr Met Cys Gly Ala Ser Leu Met Leu
 165 170 175
 Leu Leu Arg Val Glu Arg Gly Pro Gln Arg Pro Pro Pro Arg Gly Phe
 180 185 190
 Pro Gly Leu Ile Leu Leu Thr Val Leu Leu Phe Ser Ser Ala Ala Cys
 195 200 205
 Leu Arg His
 210

<210> 73
 <211> 1008
 <212> DNA
 <213> H.Sapiens

<400> 73
 atggaatcat ctttctcatt tggagtgate cttgctgtcc tggcctccct catcattgct 60
 actaacacac tagtggctgt ggctgtgctg ctgttgatcc acaagaatga tgggtgtcagt 120
 ctctgcttca ccttgaatct ggctgtggct gacaccttga ttggtgtggc catctctggc 180
 ctactcacag accagctctc cagcccttct cggcccacac agaagaccct gtgcagcctg 240
 cggatggcat ttgtcacttc ctccgcagct gcctctgtcc tcacggtcac gctgatcacc 300
 tttgacaggt accttgccat caagcagccc ttccgctact tgaagatcat gagtgggttc 360
 gtggccgggg cctgcattgc cgggctgtgg ttagtgtctt acctcattgg ctctctccca 420
 ctcggaatcc ccatgttcca gcagactgcc taaaaagggc agtgcagctt ctttgctgta 480
 tttcaccttc acttcgtgct gacctctctc tgcgttggct tcttcccage catgctcctc 540
 tttgtcttct tctactgcga catgctcaag attgcctcca tgcacagcca gcagattcga 600
 aagatggaac atgcaggagc catggctgga gggttatcga cccacaggac tcccagcgac 660
 ttcaaagctc tccgtactgt gtctgttctc attgggagct ttgctctatc ctggaccccc 720
 ttcttatca ctggcattgt gcaggtggcc tgccaggagt gtcacctcta cctagtgtgtg 780
 gaacgggtacc tgtggctgct cggcgtgggc aactccctgc tcaaccact catctatgcc 840
 tattggcaga aggaggtgcg actgcagctc taccacatgg ccctaggagt gaagaaggtg 900
 ctcacctcat tctctctctt tctctcggcc aggaattgtg gccagagag gccagggaa 960
 agttcctgtc acatcgtcac tatctccage tcagagtttg atggctaa 1008

<210> 74
 <211> 335
 <212> PRT
 <213> H.Sapiens

<400> 74

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Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala Ser
1      5      10      15
Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu Leu
20      25      30
Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala
35      40      45
Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp
50      55      60
Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu
65      70      75      80
Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val
85      90      95
Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg
100     105     110
Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly
115     120     125
Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro
130     135     140
Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val
145     150     155     160
Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro
165     170     175
Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala
180     185     190
Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met
195     200     205
Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu
210     215     220
Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro
225     230     235     240
Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu
245     250     255
Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser
260     265     270
Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu
275     280     285
Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe
290     295     300

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Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu
 305 310 315 320

Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly
 325 330 335

<210> 75
 <211> 2137
 <212> DNA
 <213> H.Sapiens

<400> 75
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 aagcgttgca tcctgttacc tggagaccct ctgagctctc acctgctact tctgccgtg 180
 cttctgcaca gagcccgggc gaggaccctt ccaggatgca ggtcccgaac agcaccggcc 240
 cggacaacgc gacgtgcag atgctgcgga acccggcgat cgcggtggcc ctgcccgtgg 300
 tgtactcgct ggtggcggcg gtcagcatcc cgggcaacct cttctctctg tgggtgctgt 360
 gccggcgcat ggggccaga tcccgcgtcg tcatcttcat gatcaacctg agcgtcacgg 420
 acctgatgct ggccagcgtg ttgcctttcc aaatctacta ccattgcaac cgccaccact 480
 ggggtattcgg ggtgctgctt tgcaacgtgg tgaccgtggc cttttacgca aacatgtatt 540
 ccagcatcct caccatgacc tgtatcagcg tggagcgctt cctgggggtc ctgtaccgcg 600
 tcagctcaa gcgctggcg cgccgtcggt acgcggtggc cgcgtgtgca gggacctggc 660
 tgctgctcct gaccgcctg tcccgcgtgg cgcgcaccga tctcacctac ccggtgcaog 720
 ccctgggcat catcacctgc ttcgacgtcc tcaagtggac gatgctcccc agcgtggcca 780
 tgtgggcccgt gttcctcttc accatcttca tcctgctggt cctcatcccg ttctgatca 840
 ccgtggcttg ttacacggcc accatcctca agctgttgcg cacggaggag gcgcacggcc 900
 gggagcagcg gaggcgcgcg gtgggcctgg ccgcggtggt cttgctggcc tttgtcacct 960
 gcttcgcccc caacaacttc gtgctcctgg cgcacatcgt gagccgcctg ttctacggca 1020
 agagctacta ccacgtgtac aagctcacgc tgtgtctcag ctgcctcaac aactgtctgg 1080
 acccgtttgt ttattacttt gcgtcccggg aattccagct gcgcctgcgg gaatatttgg 1140
 gctgccgccg ggtgccaga gacaccctgg acacgcgccg cgagagcctc ttctccgcca 1200
 ggaccacgtc cgtgcgctcc gaggccggtg cgcaccctga agggatggag ggagccacca 1260
 ggccccgcct ccagaggcag gagagtgtgt tctgagtccc gggggcgag cttggagagc 1320
 cgggggagca gcttgaggga tccagggcg catggagagg ccacggtgcc agaggttcag 1380
 ggagaacagc tgcgttgctc ccaggcactg cagaggcccg gtggggaagg gtctccaggc 1440

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tttattcctc ccaggcactg cagaggcacc ggtgaggaag ggtctccagg cttcactcag 1500
ggtagagaaa caagcaaagc ccagcagcgc acaggggtgt tggtatcctg cagaggggtgc 1560
ctctgectct ctgtgtcagg ggacagcttg tgtcaccacg cccggctaata ttttgtattt 1620
tttttagtag agctgggctg tcacccccga gtccttaga cactcctcac acctgtccat 1680
acccgaggat ggatattcaa ccagccccac cgctaccgg actcggtttc tggatatact 1740
ctgtggggcga actgcgagcc ccattcccag ctcttctccc tgctgacatc gtcccttagc 1800
acacctgtcc ataccggagg atggatattc aaccagcccc accgcctacc cgactcgggt 1860
tctggatata ctctgtgggc gaactgcgag cccattccc agctcttctc cctgctgaca 1920
tcgtccctta gttgtggttc tggccttctc cattctctc caggggttct ggtctccgta 1980
gcccgggtgca cgccgaaatt tctgtttatt tcaactcagg gcaactgtgt tgctgtggtt 2040
ggaattcttc tttcagagga gcgcctgggg ctctgcaag tcagctactc tccgtgccca 2100
cttccctca cacacacacc cccctcgtgc cgaattc 2137

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<210> 76
 <211> 359
 <212> PRT
 <213> H.Sapiens

<400> 76

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Met Gln Val Pro Asn Ser Thr Gly Pro Asp Asn Ala Thr Leu Gln Met
1          5          10          15
Leu Arg Asn Pro Ala Ile Ala Val Ala Leu Pro Val Val Tyr Ser Leu
20        25        30
Val Ala Ala Val Ser Ile Pro Gly Asn Leu Phe Ser Leu Trp Val Leu
35        40        45
Cys Arg Arg Met Gly Pro Arg Ser Pro Ser Val Ile Phe Met Ile Asn
50        55        60
Leu Ser Val Thr Asp Leu Met Leu Ala Ser Val Leu Pro Phe Gln Ile
65        70        75        80
Tyr Tyr His Cys Asn Arg His His Trp Val Phe Gly Val Leu Leu Cys
85        90        95
Asn Val Val Thr Val Ala Phe Tyr Ala Asn Met Tyr Ser Ser Ile Leu
100       105       110
Thr Met Thr Cys Ile Ser Val Glu Arg Phe Leu Gly Val Leu Tyr Pro
115       120       125
Leu Ser Ser Lys Arg Trp Arg Arg Arg Arg Tyr Ala Val Ala Ala Cys
130       135       140

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Ala Gly Thr Trp Leu Leu Leu Leu Thr Ala Leu Ser Pro Leu Ala Arg
 145 150 155 160
 Thr Asp Leu Thr Tyr Pro Val His Ala Leu Gly Ile Ile Thr Cys Phe
 165 170 175
 Asp Val Leu Lys Trp Thr Met Leu Pro Ser Val Ala Met Trp Ala Val
 180 185 190
 Phe Leu Phe Thr Ile Phe Ile Leu Leu Phe Leu Ile Pro Phe Val Ile
 195 200 205
 Thr Val Ala Cys Tyr Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu
 210 215 220
 Glu Ala His Gly Arg Glu Gln Arg Arg Arg Ala Val Gly Leu Ala Ala
 225 230 235 240
 Val Val Leu Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val
 245 250 255
 Leu Leu Ala His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr
 260 265 270
 His Val Tyr Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu
 275 280 285
 Asp Pro Phe Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu
 290 295 300
 Arg Glu Tyr Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr
 305 310 315 320
 Arg Arg Glu Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu
 325 330 335
 Ala Gly Ala His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu
 340 345 350
 Gln Arg Gln Glu Ser Val Phe
 355

<210> 77
 <211> 1197
 <212> DNA
 <213> H.Sapiens

<400> 77
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 tacaccggca agctccgcgg tgcgcgtac cagccgggtg ccggcctgcg cgcgcagccc 120
 gtgggtgtgcc tggcgggtgtg cgccttcac gtgctagaga atctagccgt gttgttggtg 180
 ctcggacgcc accgcgcgtt ccacgctccc atgttctctgc tcttgggcag cctcacgttg 240
 tcggatctgc tggcagggcg cgctacgcc gccaacatcc tactgtcggg gccgctcacg 300

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ctgaaactgt cccccgcgt ctggttcgca cgggagggag gcgtcttcgt ggcactcact    360
gcgtccgtgc tgagcctcct ggccatcgcg ctggagcgca gcctcaccat ggcgcgcagg    420
gggcccgcgc ccgtctccag tcggggggcg acgctggcga tggcagccgc ggcctggggc    480
gtgtcgctgc tctcggggt cctgccagcg ctgggctgga attgcctggg tcgcctggac    540
gcttgctcca ctgtcttgcc gctctacgcc aaggcctacg tgctcttctg cgtgctcgcc    600
ttcgtgggca tcttgccgc tatctgtgca ctctacgcgc gcatctactg ccaggtagcg    660
gccaacgcgc ggcgcctgcc ggcacggccc gggactgcgg ggaccacctc gaccgcggcg    720
cgctcgcaagc cgcgctcgct ggccttgctg cgcacgctca gcgtggtgct cctggccttt    780
gtggcatgtt ggggccccct ctctctgctg ctgttgctcg acgtggcgtg cccggcgcgc    840
acctgtcctg tactcctgca ggccgatccc ttctggggac tggccatggc caactcactt    900
ctgaacccca tcatctacac gctcaccaac cgcgacctgc gccacgcgct cctgcgcctg    960
gtctgctgcg gacgccactc ctgcggcaga gacccgagtg gctcccagca gtcggcgagc   1020
gcggctgagg ctccggggg cctgcgccgc tgctgcccc cgggccttga tgggagcttc   1080
agcggtcgg agcgctcatc gccccagcgc gacgggctgg acaccagcgg ctccacaggc   1140
agccccggtg caccacagc cgcccggact ctggtatcag aaccggctgc agactga     1197

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<210> 78
 <211> 398
 <212> PRT
 <213> H.Sapiens

<400> 78

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Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val
1           5           10          15
Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro
20          25          30
Gly Ala Gly Leu Arg Ala Asp Ala Val Val Cys Leu Ala Val Cys Ala
35          40          45
Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His
50          55          60
Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu
65          70          75          80
Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala Ala Asn Ile Leu Leu Ser
85          90          95
Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu
100         105         110

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Gly Gly Val Phe Val Ala Leu Thr Ala Ser Val Leu Ser Leu Leu Ala
 115 120 125
 Ile Ala Leu Glu Arg Ser Leu Thr Met Ala Arg Arg Gly Pro Ala Pro
 130 135 140
 Val Ser Ser Arg Gly Arg Thr Leu Ala Met Ala Ala Ala Ala Trp Gly
 145 150 155 160
 Val Ser Leu Leu Leu Gly Leu Leu Pro Ala Leu Gly Trp Asn Cys Leu
 165 170 175
 Gly Arg Leu Asp Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys Ala
 180 185 190
 Tyr Val Leu Phe Cys Val Leu Ala Phe Val Gly Ile Leu Ala Ala Ile
 195 200 205
 Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln Val Arg Ala Asn Ala Arg
 210 215 220
 Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly Thr Thr Ser Thr Arg Ala
 225 230 235 240
 Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu Arg Thr Leu Ser Val Val
 245 250 255
 Leu Leu Ala Phe Val Ala Cys Trp Gly Pro Leu Phe Leu Leu Leu Leu
 260 265 270
 Leu Asp Val Ala Cys Pro Ala Arg Thr Cys Pro Val Leu Leu Gln Ala
 275 280 285
 Asp Pro Phe Leu Gly Leu Ala Met Ala Asn Ser Leu Leu Asn Pro Ile
 290 295 300
 Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg His Ala Leu Leu Arg Leu
 305 310 315 320
 Val Cys Cys Gly Arg His Ser Cys Gly Arg Asp Pro Ser Gly Ser Gln
 325 330 335
 Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly Gly Leu Arg Arg Cys Leu
 340 345 350
 Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly Ser Glu Arg Ser Ser Pro
 355 360 365
 Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser Thr Gly Ser Pro Gly Ala
 370 375 380
 Pro Thr Ala Ala Arg Thr Leu Val Ser Glu Pro Ala Ala Asp
 385 390 395

<210> 79
 <211> 1041
 <212> DNA
 <213> H.Sapiens

<400> 79
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 ctgctcattg tggcctttgt gctgggcgca ctaggcaatg gggtcgccct gtgtggtttc 120
 tgcttcacaca tgaagacctg gaagcccagc actgtttacc ttttcaattt ggccgtggct 180
 gatttcctcc ttatgatctg cctgcctttt cggacagact attacctcag acgtagacac 240
 tgggcttttg gggacattcc ctgccgagtg gggctcttca cgttggccat gaacagggcc 300
 gggagcatcg tgttccttac ggtgggtggct gcggacaggt atttcaaagt ggtccacccc 360
 caccacgcgg tgaacactat ctccacccgg gtggcggctg gcacgtctctg caccctgtgg 420
 gccctgggtca tcctgggaac agtgtatctt ttgctggaga accatctctg cgtgcaagag 480
 aaggccgtct cctgtgagag cttcatcatg gagtcggcca atggctggca tgacatcatg 540
 ttccagctgg agttctttat gccctcggc atcatcttat ttgctcctt caagattggt 600
 tggagcctga ggcggaggca gcagctggcc agacaggctc ggatgaagaa ggcgacccgg 660
 ttcatcatgg tgggtggcaat tgtgttcac acatgctacc tgcccagcgt gtctgctaga 720
 ctctatttcc tctggacggt gccctcgagt gcctgcgac cctctgtcca tggggccctg 780
 cacataaccc tcagcttcac ctacatgaac agcatgctgg atcccctggt gtattatttt 840
 tcaagcccct cctttcccaa attctacaac aagctcaaaa tctgcagtct gaaacccaag 900
 cagccaggac actcaaaaac acaaaggccg gaagagatgc caatttcgaa cctcggtcgc 960
 aggagttgca tcagtgtggc aaatagtttc caaagccagt ctgatgggca atgggatccc 1020
 cacattgttg agtggcactg a 1041

<210> 80
 <211> 346
 <212> PRT
 <213> H.Sapiens

<400> 80

Met Tyr Asn Gly Ser Cys Cys Arg Ile Glu Gly Asp Thr Ile Ser Gln
 1 5 10 15
 Val Met Pro Pro Leu Leu Ile Val Ala Phe Val Leu Gly Ala Leu Gly
 20 25 30
 Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys
 35 40 45
 Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
 50 55 60
 Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His
 65 70 75 80

Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala
 85 90 95
 Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp
 100 105 110
 Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser
 115 120 125
 Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile
 130 135 140
 Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu
 145 150 155 160
 Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp
 165 170 175
 His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile
 180 185 190
 Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln
 195 200 205
 Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val
 210 215 220
 Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg
 225 230 235 240
 Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val
 245 250 255
 His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met
 260 265 270
 Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe
 275 280 285
 Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His
 290 295 300
 Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg
 305 310 315 320
 Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly
 325 330 335
 Gln Trp Asp Pro His Ile Val Glu Trp His
 340 345

<210> 81
 <211> 2525
 <212> DNA
 <213> H.Sapiens

<400> 81
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60

gcgacccctat agtgacaccc cacttaataca gcctctactt catagtgtctt attggcgggc	120
tggtgggtgt catttccatt cttttcctcc tggtgaaaat gaacacccgg tcagtgaacca	180
ccatggcggg cattaacttg gtggtggtcc acagcgtttt tctgctgaca gtgccatttc	240
gcttgacctt cctcatcaag aagacttgga tgtttgggct gcccttcgc aaatttgatga	300
gtgccatgct gcacatccac atgtacctca cgttcctatt ctatgtggtg atcctggtca	360
ccagatacct catcttcttc aagtgcacaa acaaagtggga attctacaga aaactgcatg	420
ctgtggctgc cagtgtggc atgtggacgc tgggtgattgt cattgtggta cccctggttg	480
tctcccggtt tggaatccat gaggaatata atgaggagca ctgttttaaa tttcacaag	540
agcttgctta cacatatgtg aaaatcatca actatatgat agtcattttt gtcatagccg	600
ttgctgtgat tctgttggtc ttccagggtc tcatcattat gttgatggtg cagaagctac	660
gccactcttt actatccac caggagttct gggctcagct gaaaaaccta ttttttatag	720
gggtcatcct tgtttgtttc cttccctacc agttcttttag gatctattac ttgaatggtg	780
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tcatatttgc ttcttttata ttgggaataa aaatgggtat aggggaggta agaatggtat	1020
ttcattactt gatcaaaacc atgccttgat gtacccaaaa caaaaggact ataaaatgca	1080
agagccctca ttgtagtctt tatgggatcc ctcccatctc tgagtgatgg ccgtacaaag	1140
accagtgttg ttgaatccac ctggagttgc aatattacat tattttccag tacagaatgt	1200
ctgtgtggcc catgaaagca acatagggtt taagagtttt agagtttcat tagctcattc	1260
taagttcctc tgtttgaagc atgggtctctt aggttttgga ctgaactcag acctttagtt	1320
cttttcatcc cacttcacct taggtaagta aattctggcc accaccacgc tccaaagaca	1380
caaactctcc ttcgctaacc aggttagatg tccattcat ctcatgccct gataaaaact	1440
gataagggga gagaatagtt aaaaattttt ctagggtatc ataactctgg taggaagtca	1500
tctgtctaga aatcaagaga aaaagaacgt gtggcctcct gttataacaa gggtttctag	1560
atttgtcctg tgaaaggctg tttaaggact tggggatcaa cttcctcaat tatcaccaat	1620
tgcactgttg ctccaaaaat catttaaaag cttactggac atatctacat aatggtgaaa	1680
ctgtaattta gagactatcc ctgactaatg tgctggtagg cattaaaatg agttcccaag	1740
ggaagtgatt aaaaattttt tctcttctgt tttttgagag aatttctaga tgtcctgggc	1800

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cacagttaat taagattttt aggggggaca gaaagttata ctgaaatctt tagagctccc 1860
ttccgccgtt aaaattatat atatatatat ttaaattata ccttaagttc tgggggtacat 1920
gtgcagaatg tgcaggtttg ttacataggt atacacgtgc catggtgggt tgcggcacct 1980
gtcaacccat ctacattagg tattttctct aatgctctcc ctcccctagc cccccacccc 2040
tggacaggcc ccattgtgtg atgttcccct ccctgtgtcc atgtgttttc attgttcaac 2100
tcccacttct aagtgagaac atgcggtgtt tggttttctg ttctgtgtt agtttgtctga 2160
gaatgatggt ttccaggtta aaattatata tttttaaata aatgaaaact gtgtttttaa 2220
aagaggactt ttgagaagta tatagaaaaa ccattaattt agactctgtg agattaggtt 2280
gcatgaagaa ggttttctga atatttgaag agtggataaa taaatgtccc ccaaagcaat 2340
aaaatcataa tccttttaaaa tataggaaaa ataactaatg ggaactaggc ttaatactcg 2400
ggatgaaata atctgtacaa caaactccca tgacacatgt ttacctatgt aacaaacctg 2460
cacatgtacc cctgaactta aaataaaatt taaagtataa taataaaata atatggattt 2520
tctttt 2525

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<210> 82
<211> 312
<212> PRT
<213> H.Sapiens

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<400> 82

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Met Thr Gly Asp Phe Pro Ser Met Pro Gly His Asn Thr Ser Arg Asn
1          5          10          15
Ser Ser Cys Asp Pro Ile Val Thr Pro His Leu Ile Ser Leu Tyr Phe
- - - - - 20          25          30
Ile Val Leu Ile Gly Gly Leu Val Gly Val Ile Ser Ile Leu Phe Leu
35          40          45
Leu Val Lys Met Asn Thr Arg Ser Val Thr Thr Met Ala Val Ile Asn
50          55          60
Leu Val Val Val His Ser Val Phe Leu Leu Thr Val Pro Phe Arg Leu
65          70          75          80
Thr Tyr Leu Ile Lys Lys Thr Trp Met Phe Gly Leu Pro Phe Cys Lys
85          90          95
Phe Val Ser Ala Met Leu His Ile His Met Tyr Leu Thr Phe Leu Phe
100         105         110
Tyr Val Val Ile Leu Val Thr Arg Tyr Leu Ile Phe Phe Lys Cys Lys
115         120         125
Asp Lys Val Glu Phe Tyr Arg Lys Leu His Ala Val Ala Ala Ser Ala

```

130 135 140
 Gly Met Trp Thr Leu Val Ile Val Ile Val Val Pro Leu Val Val Ser
 145 150 155 160
 Arg Tyr Gly Ile His Glu Glu Tyr Asn Glu Glu His Cys Phe Lys Phe
 165 170 175
 His Lys Glu Leu Ala Tyr Thr Tyr Val Lys Ile Ile Asn Tyr Met Ile
 180 185 190
 Val Ile Phe Val Ile Ala Val Ala Val Ile Leu Leu Val Phe Gln Val
 195 200 205
 Phe Ile Ile Met Leu Met Val Gln Lys Leu Arg His Ser Leu Leu Ser
 210 215 220
 His Gln Glu Phe Trp Ala Gln Leu Lys Asn Leu Phe Phe Ile Gly Val
 225 230 235 240
 Ile Leu Val Cys Phe Leu Pro Tyr Gln Phe Phe Arg Ile Tyr Tyr Leu
 245 250 255
 Asn Val Val Thr His Ser Asn Ala Cys Asn Ser Lys Val Ala Phe Tyr
 260 265 270
 Asn Glu Ile Phe Leu Ser Val Thr Ala Ile Ser Cys Tyr Asp Leu Leu
 275 280 285
 Leu Phe Val Phe Gly Gly Ser His Trp Phe Lys Gln Lys Ile Ile Gly
 290 295 300
 Leu Trp Asn Cys Val Leu Cys Arg
 305 310

<210> 83
 <211> 1125
 <212> DNA
 <213> H.Sapiens

<400> 83
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 acttctccat atgtaaataa cagcgttatg agcagcaatt catccctgct ggtggctgtg 120
 cagctgtgct acgcgaacgt gaatgggtcc tgtgtgaaaa tccccttctc gccgggatcc 180
 cgggtgattc tgtacatagt gtttggcttt ggggtgtgctc tggctgtgtt tggaaacctc 240
 ctggtgatga tttcaatcct ccatttcaag cagctgcaact ctccgaccaa ttttctcggt 300
 gcctctctgg cctgcgctga tttcttgggtg ggtgtgactg tgatgccctt cagcatggtc 360
 aggacgggtg agagctgctg gtattttggg aggagttttt gtactttcca cacctgctgt 420
 gatgtggcat tttgttactc ttctctcttt cacttgtgct tcacttccat cgacaggtac 480
 attgcgggta ctgacccccct ggtctatcct accaagttca ccgtatctgt gtcaggaatt 540


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tgcacacagcg tgcctggat cctgcccctc atgtacacagcg gtgctgtgtt ctacacaggt      600
gtctatgacg atgggctgga ggaattatct gatgccctaa actgtatagg aggttgtcag      660
accgttgtaa atcaaaactg ggtgttgaca gattttctat ccttctttat acctaccttt      720
attatgataa ttctgtatgg taacatattt cttgtggcta gacgacaggc gaaaaagata      780
gaaaatactg gtagcaagac agaatcatcc tcagagagtt acaaagccag agtggccagg      840
agagagagaa aagcagctaa aaccctgggg gtcacagtgg tagcatttat gatttcatgg      900
ttaccatata gcattgattc attaatgat gcctttatgg gctttataac cctgacctgt      960
atttatgaga tttgctgttg gtgtgcttat tataactcag ccatgaatcc tttgatttat     1020
gctttatttt acccatgggt taggaaagca ataaaagtta ttgtaactgg tcaggtttta     1080
aagaacagtt cagcaacat gaatttggtt tctgaacata tataa                        1125

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<210> 84
 <211> 345
 <212> PRT
 <213> H.Sapiens

<400> 84

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Met Ser Ser Asn Ser Ser Leu Leu Val Ala Val Gln Leu Cys Tyr Ala
1          5          10          15
Asn Val Asn Gly Ser Cys Val Lys Ile Pro Phe Ser Pro Gly Ser Arg
          20          25          30
Val Ile Leu Tyr Ile Val Phe Gly Phe Gly Ala Val Leu Ala Val Phe
          35          40          45
Gly Asn Leu Leu Val Met Ile Ser Ile Leu His Phe Lys Gln Leu His
          50          55          60
Ser Pro Thr Asn Phe Leu Val Ala Ser Leu Ala Cys Ala Asp Phe Leu
65          70          75          80
Val Gly Val Thr Val Met Pro Phe Ser Met Val Arg Thr Val Glu Ser
          85          90          95
Cys Trp Tyr Phe Gly Arg Ser Phe Cys Thr Phe His Thr Cys Cys Asp
          100          105          110
Val Ala Phe Cys Tyr Ser Ser Leu Phe His Leu Cys Phe Ile Ser Ile
          115          120          125
Asp Arg Tyr Ile Ala Val Thr Asp Pro Leu Val Tyr Pro Thr Lys Phe
          130          135          140
Thr Val Ser Val Ser Gly Ile Cys Ile Ser Val Ser Trp Ile Leu Pro
145          150          155          160
Leu Met Tyr Ser Gly Ala Val Phe Tyr Thr Gly Val Tyr Asp Asp Gly

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<210> 85
<211> 1020
<212> DNA
<213> H.Sapiens
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<400> 85						
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gcttttggaa	attgcaactga	tgaaaacatc	ccactcaaga	tgcactacct	ccctgttatt	120
tatggcatta	tcttcctcgt	gggatttcca	ggcaatgcag	tagtgatatc	cacttacatt	180
ttcaaaatga	gaccttggaa	gagcagcacc	atcattatgc	tgaacctggc	ctgcacagat	240
ctgctgtatc	tgaccagcct	ccccttcctg	attcaactact	atgccagtg	cgaaaactgg	300
atcttttgag	atttcatgtg	taagtttatc	cgcttcagct	tccatttcaa	cctgtatagc	360
agcatcctct	tcctcacctg	tttcagcatc	ttccgctact	gtgtgatcat	tcacccaatg	420
agctgctttt	ccattcacaa	aactcgatgt	gcagttgtag	cctgtgctgt	ggtgtggatc	480
atttcaactg	tagctgtcat	tccgatgacc	ttcttgatca	catcaaccaa	caggaccaac	540

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agatcagcct gtctcgacct caccagttcg gatgaactca atactattaa gtggtacaac      600
ctgattttga ctgcaagtac tttctgcctc cccttggtga tagtgacact ttgctatacc      660
acgattatcc acactttgac ccatggactg caaactgaca gctgccttaa gcagaaagca      720
cgaaggctaa ccattctgct actccttgca ttttacgtat gttttttacc cttccatata      780
ttgagggtca ttcaggatcg aatctcagcc tgctttcaat cagttgttcc attgagaatc      840
agatccatga agcttacatc gtttctagac cattatgctg ctctgaacac ctttggtaac      900
ctgttactat atgtggtggt cagcgacaac tttcagcagg ctgtctgctc aacagtgaga      960
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<210> 86
 <211> 336
 <212> PRT
 <213> H.Sapiens

<400> 86

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Met Asn Glu Pro Leu Asp Tyr Leu Ala Asn Ala Ser Asp Phe Pro Asp
1          5          10          15
Tyr Ala Ala Ala Phe Gly Asn Cys Thr Asp Glu Asn Ile Pro Leu Lys
          20          25          30
Met His Tyr Leu Pro Val Ile Tyr Gly Ile Ile Phe Leu Val Gly Phe
          35          40          45
Pro Gly Asn Ala Val Val Ile Ser Thr Tyr Ile Phe Lys Met Arg Pro
          50          55          60
Trp Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala Cys Thr Asp Leu
65          70          75          80
Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly
          85          90          95
Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Ser
          100          105          110
Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser
          115          120          125
Ile Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe Ser Ile
          130          135          140
His Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val Val Trp Ile Ile
145          150          155          160
Ser Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser Thr Asn
          165          170          175
Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Glu Leu
          180          185          190

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Asn Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Ser Thr Phe Cys
 195 200 205
 Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr
 210 215 220
 Leu Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys Gln Lys Ala Arg
 225 230 235 240
 Arg Leu Thr Ile Leu Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro
 245 250 255
 Phe His Ile Leu Arg Val Ile Gln Asp Arg Ile Ser Ala Cys Phe Gln
 260 265 270
 Ser Val Val Pro Leu Arg Ile Arg Ser Met Lys Leu Thr Ser Phe Leu
 275 280 285
 Asp His Tyr Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val
 290 295 300
 Val Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys
 305 310 315 320
 Lys Val Ser Gly Asn Leu Glu Gln Ala Lys Lys Ile Ser Tyr Ser Asn
 325 330 335

<210> 87
 <211> 1138
 <212> DNA
 <213> H.Sapiens

<400> 87
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 tgatttactc ttttattttt cctcctaggt ttctgggata agtatgtgca aataaaaaat 180
 aaacatgaga aggaactgta acctgattat ggatttgga aaaagataaa tcaacacaca 240
 aagggaaaag taaactgatt gacagccctc aggaatgatg cccttttgcc acaatataat 300
 taatatttcc tgtgtgaaaa acaactggtc aaatgatgtc cgtgcttccc tgtacagttt 360
 aatggtgctc ataattctga ccacactcgt tggcaatctg atagttattg tttctatatc 420
 acatttcaa caacttcata cccaacaaa ttggctcatt cattccatgg ccaactgtgga 480
 ctttcttctg ggggtgtctg tcatgcctta cagtatggtg agatctgctg agcactgttg 540
 gtattttgga gaagtcttct gtaaaattca cacaagcacc gacattatgc tgagctcagc 600
 ctccattttc catttgtctt tcatctccat tgaccgctac tatgctgtgt gtgatccact 660
 gagatataaa gccaaatga atatcttggt tatttgtgtg atgatcttca ttagttggag 720
 tgtccctgct gtttttgcatt ttggaatgat ctttctggag ctaaaacttca aaggcgctga 780

agagatatat tacaacatg ttactgcag aggaggttgc tctgtcttct ttagcaaaat 840
 atctggggta ctgaccttta tgacttcttt ttatatacct ggatctatta tgttatgtgt 900
 ctattacaga atatatctta tcgctaaaga acaggcaaga ttaattagtg atgccaatca 960
 gaagctccaa attggattgg aaatgaaaaa tggaatttca caaagcaaag aaaggaaagc 1020
 tgtgaagaca ttggggattg tgatgggagt tttcctaata tgctgggtgcc ctttctttat 1080
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<210> 88
 <211> 296
 <212> PRT
 <213> H.Sapiens

<400> 88

Met Met Pro Phe Cys His Asn Ile Ile Asn Ile Ser Cys Val Lys Asn
 1 5 10 15
 Asn Trp Ser Asn Asp Val Arg Ala Ser Leu Tyr Ser Leu Met Val Leu
 20 25 30
 Ile Ile Leu Thr Thr Leu Val Gly Asn Leu Ile Val Ile Val Ser Ile
 35 40 45
 Ser His Phe Lys Gln Leu His Thr Pro Thr Asn Trp Leu Ile His Ser
 50 55 60
 Met Ala Thr Val Asp Phe Leu Leu Gly Cys Leu Val Met Pro Tyr Ser
 65 70 75 80
 Met Val Arg Ser Ala Glu His Cys Trp Tyr Phe Gly Glu Val Phe Cys
 85 90 95
 Lys Ile His Thr Ser Thr Asp Ile Met Leu Ser Ser Ala Ser Ile Phe
 100 105 110
 His Leu Ser Phe Ile Ser Ile Asp Arg Tyr Tyr Ala Val Cys Asp Pro
 115 120 125
 Leu Arg Tyr Lys Ala Lys Met Asn Ile Leu Val Ile Cys Val Met Ile
 130 135 140
 Phe Ile Ser Trp Ser Val Pro Ala Val Phe Ala Phe Gly Met Ile Phe
 145 150 155 160
 Leu Glu Leu Asn Phe Lys Gly Ala Glu Glu Ile Tyr Tyr Lys His Val
 165 170 175
 His Cys Arg Gly Gly Cys Ser Val Phe Phe Ser Lys Ile Ser Gly Val
 180 185 190
 Leu Thr Phe Met Thr Ser Phe Tyr Ile Pro Gly Ser Ile Met Leu Cys
 195 200 205

Val Tyr Tyr Arg Ile Tyr Leu Ile Ala Lys Glu Gln Ala Arg Leu Ile
 210 215 220
 Ser Asp Ala Asn Gln Lys Leu Gln Ile Gly Leu Glu Met Lys Asn Gly
 225 230 235 240
 Ile Ser Gln Ser Lys Glu Arg Lys Ala Val Lys Thr Leu Gly Ile Val
 245 250 255
 Met Gly Val Phe Leu Ile Cys Trp Cys Pro Phe Phe Ile Cys Thr Val
 260 265 270
 Met Asp Pro Phe Leu His Tyr Ile Ile Pro Pro Thr Leu Asn Asp Ala
 275 280 285
 Arg Gly Ser Arg Ala Asn Ser Ala
 290 295

<210> 89
 <211> 1023
 <212> DNA
 <213> H.Sapiens

<400> 89
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 aatgatgtcc gtgcttcct gtacagttta atggtgctca taattctgac cacactcggt 120
 ggcaatctga tagttattgt ttctatatca cacttcaaac aacttcatac cccaacaaat 180
 tggctcattc attccatggc cactgtggac tttcttctgg ggtgtctggt catgccttac 240
 agtatgggtga gatctgctga gcaactgttg tattttggag aagtcttctg taaaattcac 300
 acaagcaccg acattatgct gagctcagcc tccattttcc atttgtcttt catctccatt 360
 gaccgctact atgctgtgtg tgatccactg agatataaag ccaagatgaa tatcttggtt 420
 atttgtgtga tgatcttcat tagttggagt gtccctgctg tttttgcatt tggaatgatc 480
 tttctggagc taaacttcaa aggcgctgaa gagatatatt acaaacatgt tcaactgcaga 540
 ggaggttgct ctgtcttctt tagcaaaata tctggggtac tgacctttat gacttctttt 600
 tatataacctg gatctattat gttatgtgtc tattacagaa tatatcttat cgctaaagaa 660
 caggcaagat taattagtga tgccaatcag aagctccaaa ttggattgga aatgaaaaat 720
 ggaatttcac aaagcaaaga aaggaaagct gtgaagacat tggggattgt gatgggagtt 780
 ttctaatat gctgggtgcc tttctttatc tgtacagtca tggacctttt tcttcactac 840
 attattccac ctactttgaa tgatgtattg atttggttg gctacttgaa ctctacattt 900
 aatccaatgg tttatgcatt tttctatcct tgggttagaa aagcactgaa gatgatgctg 960
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tag

1023

<210> 90
 <211> 339
 <212> PRT
 <213> H.Sapiens

<400> 90

Met Met Pro Phe Cys His Asn Ile Ile Asn Ile Ser Cys Val Lys Asn
 1 5 10 15
 Asn Trp Ser Asn Asp Val Arg Ala Ser Leu Tyr Ser Leu Met Val Leu
 20 25 30
 Ile Ile Leu Thr Thr Leu Val Gly Asn Leu Ile Val Ile Val Ser Ile
 35 40 45
 Ser His Phe Lys Gln Leu His Thr Pro Thr Asn Trp Leu Ile His Ser
 50 55 60
 Met Ala Thr Val Asp Phe Leu Leu Gly Cys Leu Val Met Pro Tyr Ser
 65 70 75 80
 Met Val Arg Ser Ala Glu His Cys Trp Tyr Phe Gly Glu Val Phe Cys
 85 90 95
 Lys Ile His Thr Ser Thr Asp Ile Met Leu Ser Ser Ala Ser Ile Phe
 100 105 110
 His Leu Ser Phe Ile Ser Ile Asp Arg Tyr Tyr Ala Val Cys Asp Pro
 115 120 125
 Leu Arg Tyr Lys Ala Lys Met Asn Ile Leu Val Ile Cys Val Met Ile
 130 135 140
 Phe Ile Ser Trp Ser Val Pro Ala Val Phe Ala Phe Gly Met Ile Phe
 145 150 155 160
 Leu Glu Leu Asn Phe Lys Gly Ala Glu Glu Ile Tyr Tyr Lys His Val
 165 170 175
 His Cys Arg Gly Gly Cys Ser Val Phe Phe Ser Lys Ile Ser Gly Val
 180 185 190
 Leu Thr Phe Met Thr Ser Phe Tyr Ile Pro Gly Ser Ile Met Leu Cys
 195 200 205
 Val Tyr Tyr Arg Ile Tyr Leu Ile Ala Lys Glu Gln Ala Arg Leu Ile
 210 215 220
 Ser Asp Ala Asn Gln Lys Leu Gln Ile Gly Leu Glu Met Lys Asn Gly
 225 230 235 240
 Ile Ser Gln Ser Lys Glu Arg Lys Ala Val Lys Thr Leu Gly Ile Val
 245 250 255
 Met Gly Val Phe Leu Ile Cys Trp Cys Pro Phe Phe Ile Cys Thr Val

260	265	270
Met Asp Pro Phe Leu His Tyr Ile Ile Pro Pro Thr Leu Asn Asp Val		
275	280	285
Leu Ile Trp Phe Gly Tyr Leu Asn Ser Thr Phe Asn Pro Met Val Tyr		
290	295	300
Ala Phe Phe Tyr Pro Trp Phe Arg Lys Ala Leu Lys Met Met Leu Phe		
305	310	315
Gly Lys Ile Phe Gln Lys Asp Ser Ser Arg Cys Lys Leu Phe Leu Glu		
325	330	335
Leu Ser Ser		

<210> 91
 <211> 1696
 <212> DNA
 <213> H.Sapiens

<400> 91
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 cacagcacog tctctcccat actcggatcat tcacaccatc attgattcac caggcaccac 180
 tccgtgtcca gcaggactct ggggacccca aatggacact accatggaag ctgacctggg 240
 tgccactggc cacaggcccc gcacagagct tgatgatgag gactcctacc cccaagggtg 300
 ctgggacacg gtcttctctg tggccctgct gctccttggg ctgccagcca atgggttgat 360
 ggcgtggctg gccggctccc aggcccgga tggagctggc acgcgtctgg cgctgctcct 420
 gctcagcctg gccctctctg acttcttgtt cctggcagca gcggccttcc agatcctaga 480
 gatccggcat gggggacact ggccgctggg gacagctgcc tgccgcttct actacttct 540
 atggggcgtg tctactcct ccggcctctt cctgctggcc gccctcagcc tcgaccgctg 600
 cctgctggcg ctgtgccac actggtaccc tgggcaccgc ccagtcgcc tgccctctg 660
 ggtctgcgc ggtgtctggg tgetggccac actcttcagc gtgccctggc tggctctccc 720
 cgaggctgcc gtctggtggt acgacctgt catctgctg gacttctggg acagcgagga 780
 gctgtcgtg aggatgctg aggtcctggg gggttctct cctttcctcc tgctgctcgt 840
 ctgccacgtg ctacccagg ccacagcctg tcgcacctgc caccgccaac agcagcccgc 900
 agcctgccgg ggtctgcgc gtgtggccag gaccattctg tcagcctatg tggctctgag 960
 gctgccctac cagctggccc agctgctcta cctggccttc ctgtgggacg tctactctgg 1020
 ctacctgctc tgggaggccc tggctactc cgactacctg atcctactca acagctgcct 1080

cagcccccttc ctctgcctca tggccagtgc cgacctccgg acctgtgtgc gctccgtgct 1140
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 acagatggat cctgtggccc agcctcaggt gaaccccaca ctccagccac gatcggatcc 1320
 cacagctcag ccacagctga accctacggc ccagccacag tcggatccca cagcccagcc 1380
 acagctgaac ctcatggccc agccacagtc agattctgtg gccagccac aggcagacac 1440
 taacgtccag acccctgcac ctgctgccag ttctgtgccc agtccctgtg atgaagcttc 1500
 cccaacccca tctctgcctc ctaccccagg ggcccttgag gaccagcca cacctcctgc 1560
 ctctgaagga gaaagcccca gcagcaccac gccagaggcg gcccggggcg caggccccac 1620
 gtgagggtcc aggaacacgc aggccacca gagcagtga agagcccagg gcagacagag 1680
 gaaccagcca gtcaga 1696

<210> 92
 <211> 505
 <212> PRT
 <213> H.Sapiens

<400> 92

Leu Ala Trp Arg Cys Thr Ala Pro Ser Leu Pro Tyr Ser Val Ile His
 1 5 10 15
 Thr Ile Ile Asp Ser Pro Gly Thr Thr Pro Cys Pro Ala Gly Leu Trp
 20 25 30
 Gly Pro Gln Met Asp Thr Thr Met Glu Ala Asp Leu Gly Ala Thr Gly
 35 40 45
 His Arg Pro Arg Thr Glu Leu Asp Asp Glu Asp Ser Tyr Pro Gln Gly
 50 55 60
 Gly Trp Asp Thr Val Phe Leu Val Ala Leu Leu Leu Leu Gly Leu Pro
 65 70 75 80
 Ala Asn Gly Leu Met Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly
 85 90 95
 Ala Gly Thr Arg Leu Ala Leu Leu Leu Ser Leu Ala Leu Ser Asp
 100 105 110
 Phe Leu Phe Leu Ala Ala Ala Phe Gln Ile Leu Glu Ile Arg His
 115 120 125
 Gly Gly His Trp Pro Leu Gly Thr Ala Ala Cys Arg Phe Tyr Tyr Phe
 130 135 140
 Leu Trp Gly Val Ser Tyr Ser Ser Gly Leu Phe Leu Leu Ala Ala Leu
 145 150 155 160

Ser Leu Asp Arg Cys Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly
 165 170 175
 His Arg Pro Val Arg Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val
 180 185 190
 Leu Ala Thr Leu Phe Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala
 195 200 205
 Val Trp Trp Tyr Asp Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu
 210 215 220
 Glu Leu Ser Leu Arg Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe
 225 230 235 240
 Leu Leu Leu Leu Val Cys His Val Leu Thr Gln Ala Thr Ala Cys Arg
 245 250 255
 Thr Cys His Arg Gln Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg
 260 265 270
 Val Ala Arg Thr Ile Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr
 275 280 285
 Gln Leu Ala Gln Leu Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser
 290 295 300
 Gly Tyr Leu Leu Trp Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu
 305 310 315 320
 Leu Asn Ser Cys Leu Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp
 325 330 335
 Leu Arg Thr Leu Leu Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu
 340 345 350
 Cys Glu Glu Arg Pro Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln
 355 360 365
 Leu Asp Ser Glu Gly Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln
 370 375 380
 Ser Gln Met Asp Pro Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln
 385 390 395 400
 Pro Arg Ser Asp Pro Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln
 405 410 415
 Pro Gln Ser Asp Pro Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln
 420 425 430
 Pro Gln Ser Asp Ser Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln
 435 440 445
 Thr Pro Ala Pro Ala Ala Ser Ser Val Pro Ser Pro Cys Asp Glu Ala
 450 455 460
 Ser Pro Thr Pro Ser Ser His Pro Thr Pro Gly Ala Leu Glu Asp Pro

465 470 475 480
 Ala Thr Pro Pro Ala Ser Glu Gly Glu Ser Pro Ser Ser Thr Pro Pro
 485 490 495

Glu Ala Ala Pro Gly Ala Gly Pro Thr
 500 505

<210> 93
 <211> 1413
 <212> DNA
 <213> H.Sapiens

<400> 93
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 ctccttgggc tgccagccaa tgggttgatg gcgtggctgg ccggctccca ggcccgcat 180
 ggagctggca cgcgtctggc gctgctctctg ctacagctgg cctctctctga cttcttgttc 240
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 acagctgcct gccgcttcta ctacttcta tggggcgtgt cctactcctc cggcctcttc 360
 ctgctggccg ccctcagcct cgaccgctgc ctgctggcgc tgtgccaca ctggtaccct 420
 gggcaccgcc cagtccgcct gcccctctgg gtctgcgccg gtgtctgggt gctggccaca 480
 ctcttcagcg tgccctggct ggtcttcccc gaggtgccg tctggtggta cgacctggtc 540
 atctgcctgg acttctggga cagcgaggag ctgtcgtga ggatgctgga ggtcctgggg 600
 ggcttcctgc ctttctcct gctgctcgtc tgccacgtgc tcaccagggc cacagcctgt 660
 cgcacctgcc accgccaaca gcagcccgca gcctgccggg gcttcgcccg tgtggccagg 720
 accattctgt cagcctatgt ggtcctgagg ctgccctacc agctggcca gctgctctac 780
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 gacctccgga cctgctgcg ctccgtgctc tcgtccttcg cggcagctct ctgcgaggag 960
 cggccgggca gcttcacgcc cactgagcca cagaccagc tagattctga ggtccaact 1020
 ctgccagagc cgatggcaga ggcccagtca cagatggatc ctgtggcca gcctcaggtg 1080
 aacccacac tccagccacg atcggatccc acagctcagc cacagctgaa ccctacggcc 1140
 cagccacagt cggatccac agcccagcca cagctgaacc tcatggcca gccacagtca 1200
 gactctgtgg ccagccaca ggcagacact aacgtccaga cccctgcacc tgctgccagt 1260
 tctgtgcca gtccctgtga tgaagcttcc ccaaccccat cctcgcctcc taccaggg 1320
 gcccttgagg acccagccac acctcctgcc tctgaaggag aaagcccag cagacccccg 1380

ccagaggcgg ccccgggcgc agggcccacg tga

1413

<210> 94
 <211> 419
 <212> PRT
 <213> H.Sapiens

<400> 94

Met	Asp	Thr	Thr	Met	Glu	Ala	Asp	Leu	Gly	Ala	Thr	Gly	His	Arg	Pro
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Arg	Thr	Glu	Leu	Asp	Asp	Glu	Asp	Ser	Tyr	Pro	Gln	Gly	Gly	Trp	Asp
			20					25					30		
Thr	Val	Phe	Leu	Val	Ala	Leu	Leu	Leu	Leu	Gly	Leu	Pro	Ala	Asn	Gly
		35					40					45			
Leu	Met	Ala	Trp	Leu	Ala	Gly	Ser	Gln	Ala	Arg	His	Gly	Ala	Gly	Thr
	50					55					60				
Arg	Leu	Ala	Leu	Leu	Leu	Leu	Ser	Leu	Ala	Leu	Ser	Asp	Phe	Leu	Phe
65					70					75					80
Leu	Ala	Ala	Ala	Ala	Phe	Gln	Ile	Leu	Glu	Ile	Arg	His	Gly	Gly	His
				85					90					95	
Trp	Pro	Leu	Gly	Thr	Ala	Ala	Cys	Arg	Phe	Tyr	Tyr	Phe	Leu	Trp	Gly
			100					105					110		
Val	Ser	Tyr	Ser	Ser	Gly	Leu	Phe	Leu	Leu	Ala	Ala	Leu	Ser	Leu	Asp
		115					120					125			
Arg	Cys	Leu	Leu	Ala	Leu	Cys	Pro	His	Trp	Tyr	Pro	Gly	His	Arg	Pro
	130					135					140				
Val	Arg	Leu	Pro	Leu	Trp	Val	Cys	Ala	Gly	Val	Trp	Val	Leu	Ala	Thr
145					150					155					160
Leu	Phe	Ser	Val	Pro	Trp	Leu	Val	Phe	Pro	Glu	Ala	Ala	Val	Trp	Trp
				165					170					175	
Tyr	Asp	Leu	Val	Ile	Cys	Leu	Asp	Phe	Trp	Asp	Ser	Glu	Glu	Leu	Ser
			180					185					190		
Leu	Arg	Met	Leu	Glu	Val	Leu	Gly	Gly	Phe	Leu	Pro	Phe	Leu	Leu	Leu
		195					200					205			
Leu	Val	Cys	His	Val	Leu	Thr	Gln	Ala	Thr	Ala	Cys	Arg	Thr	Cys	His
	210					215					220				
Arg	Gln	Gln	Gln	Pro	Ala	Ala	Cys	Arg	Gly	Phe	Ala	Arg	Val	Ala	Arg
225					230					235					240
Thr	Ile	Leu	Ser	Ala	Tyr	Val	Val	Leu	Arg	Leu	Pro	Tyr	Gln	Leu	Ala
				245					250					255	

Gln Leu Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu
 260 265 270
 Leu Trp Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser
 275 280 285
 Cys Leu Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr
 290 295 300
 Leu Leu Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu Cys Glu Glu
 305 310 315 320
 Arg Pro Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln Leu Asp Ser
 325 330 335
 Glu Gly Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln Ser Gln Met
 340 345 350
 Asp Pro Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln Pro Arg Ser
 355 360 365
 Asp Pro Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln Pro Gln Ser
 370 375 380
 Asp Pro Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln Pro Gln Ser
 385 390 395 400
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 405 410 415
 Pro Ala Ala

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<210> 97
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<400> 97
gctcaacc ca ctcatttatg cc 22

<210> 98
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<400> 98
aaactttctt gcccttaccg tc 22

<210> 99
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<400> 99
aaagcagcac cccgaatacc 20

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<400> 100
catgatcaac ctgagcgtca c 21

<210> 101

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28

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<210> 103
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gcacccctggc cgctatctgt gcactctacg

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<400> 104
cgtagagtgc acagatagcg gccaggatgc

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<400> 105
aaccatcatca tctacacgc 19

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<400> 106
tgcctgtgga gccgctgg 18

<210> 107
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<400> 109

gaagcccagc actgtttacc

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<400> 114
acccactta atcagcctc 19

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<400> 117
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<400> 118
ccgcaggagc aatgaaaatc ag 22

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<400> 119
ctgaaagttg tcgctgacc 19

<210> 120
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<400> 121
gcataccatg aatgagccac tagac 25

<210> 122
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<400> 123
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<400> 125
acttcaaaca acttcatacc cc 22

<210> 126
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<400> 126
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<400> 127

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<210> 129
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<400> 129

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<400> 130
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52

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<400> 131
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20

<210> 132
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<400> 132
gcgtatatac actcactata gggagacctg ccacactgat gcaactcc 48

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<212> DNA
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<220>
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<400> 133
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<210> 134
<211> 50
<212> DNA
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<400> 134
gcgtaatac actcactata gggagaccgc acgccactct ttactatccc 50

<210> 135
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<400> 135
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<400> 136
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<400> 137
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23

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<400> 138
gcgtaatagc actcactata gggagacctt atgagcagca attcatccc

49

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<400> 139
cacacccacc aagaaatcag

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<210> 140
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<400> 141
ttatgagcag caattcatcc c

21

<210> 142
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<400> 142
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<400> 143
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19

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<400> 148
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<400> 150
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<400> 153
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<400> 156
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<400> 158
gatcctcgag tcacgtgggg cctgcgcccg g

31

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<210> 184

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<400> 184

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22

<210> 185

<211> 1188

<212> DNA

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<400> 185

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ctatccaacg cactggtgct gctttgttgc gcctacagcg ctgagctccg cactcgagcc	180
tcaggcgctc tcttggtgaa tctgtctctg ggccacctgc tgctggcggc gctggacatg	240
cccttcacgc tgctcggtgt gatgcgcggg cggacaccgt cggcgccccg cgcatgccaa	300
gtcattggct tcttggaacac ctctctggcg tccaacgcgg cgctgagcgt ggcggcgctg	360
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ttcgtgctgc cgctggcggt gctctgcctc acctcgctcc aggtgcaccg ggtggcacgc	660
agacactgcc agcgcattgga caccgtcacc atgaaggcgc tcgcgctgct cgccgacctg	720
cacccagtg tgccgcagcg ctgcctcatc cagcagaagc ggcgcgccca ccgcgccacc	780
aggaagattg gcattgctat tgcgaccttc ctcatctgct ttgccccgta tgtcatgacc	840

aggctggcgg agctcgtgcc cttcgtcacc gtgaacgccc agtggggcat cctcagcaag 900
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 tccacccatg acagctctct ggatgtggcc ggcattggtgc accagctgct gaagagaacc 1080
 ccgcgcccag cgtccaccca caacggctct gtggacacag agaatgattc ctgcctgcag 1140
 cagacacact gagggcctgg cagggctcat cgccccacc ttctaaga 1188

<210> 186
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 <213> H.Sapiens

<400> 186

Met Gly Pro Gly Glu Ala Leu Leu Ala Gly Leu Leu Val Met Val Leu
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 Ser Ala Glu Leu Arg Thr Arg Ala Ser Gly Val Leu Leu Val Asn Leu
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 Ser Leu Gly His Leu Leu Leu Ala Ala Leu Asp Met Pro Phe Thr Leu
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 Leu Gly Val Met Arg Gly Arg Thr Pro Ser Ala Pro Gly Ala Cys Gln
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 Val Ile Gly Phe Leu Asp Thr Phe Leu Ala Ser Asn Ala Ala Leu Ser
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 Val Ala Ala Leu Ser Ala Asp Gln Trp Leu Ala Val Gly Phe Pro Leu
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 Arg Tyr Ala Gly Arg Leu Arg Pro Arg Tyr Ala Gly Leu Leu Leu Gly
 115 120 125
 Cys Ala Trp Gly Gln Ser Leu Ala Phe Ser Gly Ala Ala Leu Gly Cys
 130 135 140
 Ser Trp Leu Gly Tyr Ser Ser Ala Phe Ala Ser Cys Ser Leu Arg Leu
 145 150 155 160
 Pro Pro Glu Pro Glu Arg Pro Arg Phe Ala Ala Phe Thr Ala Thr Leu
 165 170 175
 His Ala Val Gly Phe Val Leu Pro Leu Ala Val Leu Cys Leu Thr Ser
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 Leu Gln Val His Arg Val Ala Arg Arg His Cys Gln Arg Met Asp Thr
 195 200 205

Val Thr Met Lys Ala Leu Ala Leu Leu Ala Asp Leu His Pro Ser Val
 210 215 220

Arg Gln Arg Cys Leu Ile Gln Gln Lys Arg Arg Arg His Arg Ala Thr
 225 230 235 240

Arg Lys Ile Gly Ile Ala Ile Ala Thr Phe Leu Ile Cys Phe Ala Pro
 245 250 255

Tyr Val Met Thr Arg Leu Ala Glu Leu Val Pro Phe Val Thr Val Asn
 260 265 270

Ala Gln Trp Gly Ile Leu Ser Lys Cys Leu Thr Tyr Ser Lys Ala Val
 275 280 285

Ala Asp Pro Phe Thr Tyr Ser Leu Leu Arg Arg Pro Phe Arg Gln Val
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Leu Ala Gly Met Val His Arg Leu Leu Lys Arg Thr Pro Arg Pro Ala
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Ser Thr His Asp Ser Ser Leu Asp Val Ala Gly Met Val His Gln Leu
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